

6-24-02 10090182 1647 1800-39



**TRANSMITTAL LETTER**  
**(General - Patent Pending)**

Docket No.  
126181-1014

In Re Application Of **Bauer, et al**

Serial No.  
10/090,182

Filing Date  
March 4, 2002

Examiner  
Unknown

Group Art Unit  
1647

Title: **METHODS OF EX-VIVO EXPANSION OF HEMATOPOIETIC CELLS USING INTERLEUKIN-3 (IL-3) MULTIPLE MUTATION POLYPEPTIDES**

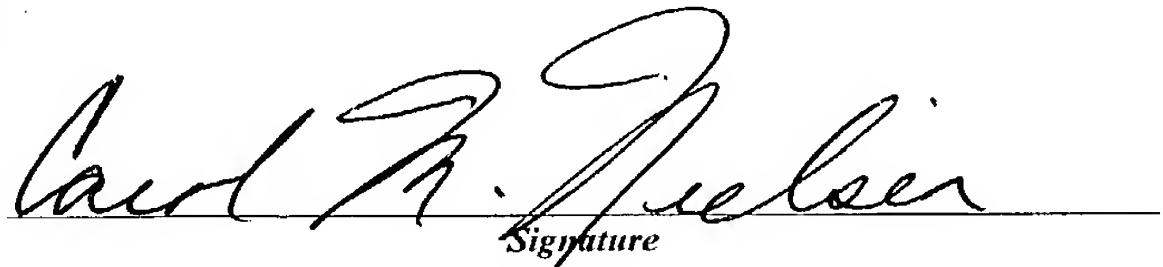
TO THE COMMISSIONER OF PATENTS AND TRADEMARKS:

Transmitted herewith is:

1. Response to Notice to Comply with Sequence Listing;
2. Copy of Notice to Comply dated May 1, 2002;
3. Statement Under 37 C.F.R. § 1.82 (f);
4. Computer Readable Form of Sequence Listing and Paper Copy of Sequence Listing;
5. Substitute Replacement Sheet and Two (2) identical compact discs; and 6. Return Postcard.

in the above identified application.

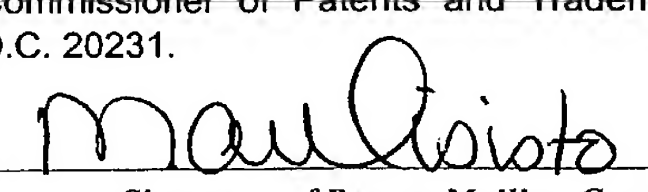
- ☒ No additional fee is required.
- ☐ A check in the amount of \_\_\_\_\_ is attached.
- ☐ The Commissioner is hereby authorized to charge and credit Deposit Account No. \_\_\_\_\_ as described below. A duplicate copy of this sheet is enclosed.
- ☐ Charge the amount of \_\_\_\_\_
  - ☐ Credit any overpayment.
  - ☐ Charge any additional fee required.

  
Signature

Carol M. Nielsen  
Registration No. 37,676  
Gardere Wynne Sewell LLP  
1601 Elm Street, Suite 3000  
Dallas, Texas 75201  
713-276-5383 phone  
713-276-5555 fax  
cnielsen@gardere.com

Dated: June 19, 2002

cc: S. Christopher Bauer

I certify that this document and fee is being deposited on <u>6-19-02</u> with the U.S. Postal Service as first class mail under 37 C.F.R. 1.8 and is addressed to the Commissioner of Patents and Trademarks, Washington, D.C. 20231.	
	
Signature of Person Mailing Correspondence	
Mark Disisto	
Typed or Printed Name of Person Mailing Correspondence	

Attorney Docket 126181-1014

PATENT



## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application Of:

Bauer, et al.

Examiner: Unknown

Serial No.: 10/090,182

Filed: March 4, 2002

For: METHOD OF EX-VIVO  
EXPANSION OF HEMATOPOIETIC  
CELLS USING INTERLEUKIN-3  
(IL-3) MULTIPLE MUTATION  
POLYPEPTIDES

## CERTIFICATE OF MAILING

I hereby certify that this document is being deposited on this  
19th day of June, 2002 with the U.S. Postal Service  
"Express Mail to Addressee" service under 37 C.F.R. 1.10 and  
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Sequence, P.O. Box 2327, Arlington, Virginia 22202.

*Mark Disisto*  
Signature of Person Mailing Correspondence

Mark Disisto  
Typed or Printed Name of Person Mailing Correspondence

EL 922861298 US  
"Express Mail" Mailing Label Number

**BOX: SEQUENCE**

United States Patent and Trademark Office  
P.O. Box 2327  
Arlington, Virginia 22202

**RESPONSE TO NOTICE TO COMPLY WITH SEQUENCE LISTING**

This is in response to the Office Action mailed on May 1, 2002. The Examiner has indicated that the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, and that a substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

**REMARKS**

Pursuant to the requirements of 37 C.F.R. 1.822, 1.823 and 1.825(d), we submit a substitute computer readable form (CRF) copy of the "Sequence Listing;" a substitute paper copy of the "Sequence Listing;" and a statement that the content of the paper and computer copies are the same, as required by 37 C.F.R. 1.821(f).

Attorney Docket 126181-1014

PATENT

**AMENDMENT TO SEQUENCE LISTING**

Pursuant to 37 C.F.R. § 1.825, Applicant submits herewith the enclosed substitute sheet amending the attorney/agent information and correspondence address. Also enclosed are two (2) copies of the replacement disc in compliance with § 1.52(e). Compact discs, copy 1 and copy 2, are identical. No new matter has been added.

**CONCLUSION**

The present paper constitutes a complete response to the Office Communication mailed May 1, 2002. Applicant respectfully requests reconsideration of the application in light of the substitutions. Applicant requests that this case be allowed and pass to issuance.

While the Applicant believes that no fees are due at this time, Applicant hereby authorizes the Commissioner to charge any fees that may be required by this paper to Deposit Account 07-0153.

Respectfully submitted,

Date: June 19, 2002By: Carol M. Nielsen  
Carol M. Nielsen  
Reg. No. 37,676

Gardere Wynne Sewell LLP  
Patent Section (H)  
1601 Elm Street, Suite 3000  
Dallas, Texas 75201-4761  
713-276-5383 phone  
713-276-5555 fax  
cnielsen@gardere.com

Attorney Docket No. 126181-1014

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In Re Application Of:

Bauer, et al

Examiner: Unknown

Serial No.: 10/090,182

Filed: March 4, 2000

For: METHOD OF EX-VIVO  
EXPANSION OF HEMATOPOIETIC  
CELLS USING INTERLEUKIN-3  
(IL-3) MULTIPLE MUTATION  
POLYPEPTIDES



CERTIFICATE OF MAILING

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"Express Mail to Addressee" service under 37 C.F.R. 1.10  
and is addressed to: U.S. Patent and Trademark Office, Box  
Sequence, P.O. Box 2327, Arlington Virginia 22202.

*Mark Disisto*

Signature of Person Mailing Correspondence

Mark Disisto

Typed or Printed Name of Person Mailing Correspondence

EL 922861298 US

"Express Mail" Mailing Label Number

**BOX: SEQUENCE**

United States Patent and Trademark Office  
P.O. Box 2327  
Arlington, Virginia 22202

STATEMENT UNDER 37 C.F.R. § 1.821(f)

Dear Sir:

This will confirm that the content of the substitute paper copy of and the substitute computer readable copy of the Sequence Listing submitted herewith are the same. Compact discs, copy 1 and copy 2, are identical. No new matter has been added.

While the Applicant believes that no fees are due at this time, Applicant hereby authorizes the Commissioner to charge any fees that may be required by this paper to Deposit Account 07-0153.

Dated this 17th day of June 2002.




Attorney Docket No.: 126181-1014

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PATENT

Respectfully submitted,

GARDERE WYNNE SEWELL LLP

By:   
Carol M. Nielsen  
Registration No.: 37,676

Carol M. Nielsen  
GARDERE WYNNE SEWELL LLP  
Patent Section (H)  
1601 Elm Street, Suite 3000  
Dallas, Texas 75201-4761  
713-276-5383 phone  
713-276-5555 fax  
cnielsen@gardere.com

Attorney Docket No. 126181-1014



## UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS  
UNITED STATES PATENT AND TRADEMARK OFFICE  
WASHINGTON, D.C. 20231  
www.uspto.gov

APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
10/090,182	03/04/2002	S. Christopher Bauer	2713/12/US

Pharmacia Corporation  
Corporate Patent Department  
800 N. Lindbergh Blvd.  
Mail Zone O4E  
St. Louis, MO 63167



CONFIRMATION NO. 5061

## FORMALITIES LETTER



\*OC000000007988908\*

Date Mailed: 05/01/2002

### NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

- For Rules Interpretation, call (703) 308-4216
- To Purchase PatentIn Software, call (703) 306-2600
- For PatentIn Software Program Help, call (703) 306-4119 or e-mail at [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or [patin3help@uspto.gov](mailto:patin3help@uspto.gov)

*A copy of this notice MUST be returned with the reply.*

Customer Service Center  
Initial Patent Examination Division (703) 308-1202

PART 2 - COPY TO BE RETURNED WITH RESPONSE

## (1) GENERAL INFORMATION:

(i) APPLICANT: Abrams, Mark A.  
Bauer, S. C.  
Braford-Goldberg, Sarah R.  
Caparon, Maire H.  
Easton, Alan M.  
Klein, Barbara K.  
McKearn, John P.  
Olins, Peter O.  
Paik, Kumnan  
Thomas, John W.

(ii) TITLE OF INVENTION: Methods of Ex-vivo Expansion of Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple Mutation Polypeptides

(iii) NUMBER OF SEQUENCES: 415

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Carol M. Nielsen  
Gardere Wynne Sewell LLP  
(B) STREET: 1601 Elm Street, Suite 3000  
(C) CITY: Dallas  
(D) STATE: Texas  
(E) COUNTRY: USA  
(F) ZIP: 75201

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 04-MAR-2002  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/764,114  
(B) FILING DATE: 09-DEC-1996

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/981,044  
(B) FILING DATE: 24-NOV-1992

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US93/11197  
(B) FILING DATE: 22-NOV-1993

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/411,795  
(B) FILING DATE: 04-JUN-1995

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Carol M. Nielsen  
(B) REGISTRATION NUMBER: 37,676  
(C) REFERENCE/DOCKET NUMBER: 126181-1014 (C2713/12)



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Abrams, Mark A.  
Bauer, S. C.  
Braford-Goldberg, Sarah R.  
Caparon, Maire H.  
Easton, Alan M.  
Klein, Barbara K.  
McKearn, John P.  
Olins, Peter O.  
Paik, Kumnun  
Thomas, John W.

(ii) TITLE OF INVENTION: Methods of Ex-vivo Expansion of Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple Mutation Polypeptides

(iii) NUMBER OF SEQUENCES: 415

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Carol M. Nielsen  
Gardere Wynne Sewell LLP  
(B) STREET: 1601 Elm Street, Suite 3000  
(C) CITY: Dallas  
(D) STATE: Texas  
(E) COUNTRY: USA  
(F) ZIP: 75201

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(B) FILING DATE: 22-NOV-1993

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/411,795  
(B) FILING DATE: 04-JUN-1995

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Carol M. Nielsen  
(B) REGISTRATION NUMBER: 36,676  
(C) REFERENCE/DOCKET NUMBER: 126181-1014 (C2713/12)

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (713)276-5383  
(B) TELEFAX: (713)276-5555



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# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Abrams, Mark A.  
Bauer, S. C.  
Braford-Goldberg, Sarah R.  
Caparon, Maire H.  
Easton, Alan M.  
Klein, Barbara K.  
McKearn, John P.  
Olins, Peter O.  
Paik, Kumnan  
Thomas, John W.

(ii) TITLE OF INVENTION: Methods of Ex-vivo Expansion of Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple Mutation Polypeptides

(iii) NUMBER OF SEQUENCES: 415

### (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: S. Christopher Bauer, Pharmacia Corp  
Corporate Patent Dept. Mail Zone 04E  
(B) STREET: 800 N. Lindbergh Blvd.  
(C) CITY: St. Louis  
(D) STATE: Missouri  
(E) COUNTRY: USA  
(F) ZIP: 63167

### (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(A) APPLICATION NUMBER: PCT/US93/11197  
(B) FILING DATE: 22-NOV-1993

### (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/411,795  
(B) FILING DATE: 04-JUN-1995

### (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: S. Christopher Bauer  
(B) REGISTRATION NUMBER: 42,305  
(C) REFERENCE/DOCKET NUMBER: C2713/12

### (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (636)737-6257  
(B) TELEFAX: (736)737-6257

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTAGCGATCT TTTAATAAGC TTG

23

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCCAAGCT TATTAAAAGA TCG

23

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 69 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCAACAATT TCTACAAAAC ACTTGATACT GTATGAGCAT ACAGTATAAT TGCTTCAACA

60

GAACAGATC

69

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 67 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGTTCTGTTG AAGCAATTAT ACTGTATGCT CATAAGTAT CAAGTGTTTT GTAGAAATTG

60

TTGCCGC

67

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCATTGCTGC CGGCATCGTG GTC

23

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 46 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CATGGCTCCA ATGACTCAGA CTA CTCTCT TAAGACTTCT TGGGTT

46

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AACCCAAGAA GTCTTAAGAG AAGTAGTCTG AGTCATTGGA GC

42

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 64 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AATTCCGTCG TAACTGACC TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT

60



AATA

64

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 64 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGCTTATTAC TGTTGAGCCT GCGCGTTCTC CAAGGTTTTC AGATAGAAGG TCAGTTTACG 60  
ACGG 64

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 126 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	
1				5					10					15		
Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro	Pro	
			20					25					30			
Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp	Ile	
			35				40					45				
Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn	Arg	
			50			55					60					
Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	Lys	
65					70					75					80	
Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	His	
				85					90					95		
Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys	Leu	
				100				105					110			
Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln			
			115				120					125				

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CATGGCTAAC TGCTCTAACA TGAT

24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGATCATGTT AGAGCAGTTA GC

22

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ala	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	1	5	10	15
Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	20	25	30	
Gln	Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	35	40	45	
Phe	Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	50	55	60	
Ile	Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Thr	Arg	His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	85	90	95	
Arg	Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	100	105	110	
Gln																			

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Met	Ile	Thr	Leu	Arg	Lys	Leu	Pro	Leu	Ala	Val	Ala	Val	Ala	Ala
1				5					10					15	

Gly	Val	Met	Ser	Ala	Gln	Ala	Met	Ala	Asn	Cys
			20				25			

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /note= "Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /note= "Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 22
- (D) OTHER INFORMATION: /note= "Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val,

or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile, Val, Ala, Leu, Gly, Trp, Lys, Phe, Ser, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 24
- (D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 26
- (D) OTHER INFORMATION: /note= "Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 27
- (D) OTHER INFORMATION: /note= "Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 28
- (D) OTHER INFORMATION: /note= "Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 31
- (D) OTHER INFORMATION: /note= "Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 33

(D) OTHER INFORMATION: /note= "Xaa at position 33 is Pro,  
Leu, Gln, Ala, Thr, or Glu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 34  
(D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu,  
Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe,  
Ile, or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 35  
(D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu,  
Ala, Gly, Asn, Pro, Gln, or Val"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 36  
(D) OTHER INFORMATION: /note= "Xaa at position 36 is Asp,  
Leu, or Val"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 37  
(D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe,  
Ser, Pro, Trp, or Ile"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 38  
(D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn,  
or Ala"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 40  
(D) OTHER INFORMATION: /note= "Xaa at position 40 is Leu,  
Trp, or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 41  
(D) OTHER INFORMATION: /note= "Xaa at position 41 is Asn,  
Cys, Arg, Leu, His, Met, or Pro"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 42  
(D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,  
Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr,  
Ile, Met, or Ala"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 43  
(D) OTHER INFORMATION: /note= "Xaa at position 43 is Glu,  
Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr, Gly,  
or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 44  
(D) OTHER INFORMATION: /note= "Xaa at position 44 is Asp,  
Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala,  
or Pro"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 45  
 (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,  
 Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg,  
 Ser, Ala, Ile, Glu, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 46  
 (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp,  
 Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr,  
 Ile, Val, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 47  
 (D) OTHER INFORMATION: /note= "Xaa at position 47 is Ile,  
 Gly, Val, Ser, Arg, Pro, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 48  
 (D) OTHER INFORMATION: /note= "Xaa at position 48 is Leu,  
 Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met,  
 Val, or Asn"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 49  
 (D) OTHER INFORMATION: /note= "Xaa at position 49 is Met,  
 Arg, Ala, Gly, Pro, Asn, His, or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 50  
 (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu,  
 Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His,  
 Phe, Met, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 51  
 (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn,  
 Arg, Met, Pro, Ser, Thr, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 52  
 (D) OTHER INFORMATION: /note= "Xaa at position 52 is Asn,  
 His, Arg, Leu, Gly, Ser, or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 53  
 (D) OTHER INFORMATION: /note= "Xaa at position 53 is  
 Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 54  
 (D) OTHER INFORMATION: /note= "Xaa at position 54 is Arg,  
 Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala,  
 or Leu"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 55  
 (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg,  
 Thr, Val, Ser, Leu, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 56  
 (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro,  
 Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr,  
 Phe, Leu, Val, or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 57  
 (D) OTHER INFORMATION: /note= "Xaa at position 57 is Asn  
 or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 58  
 (D) OTHER INFORMATION: /note= "Xaa at position 58 is Leu,  
 Ser, Asp, Arg, Gln, Val, or Cys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 59  
 (D) OTHER INFORMATION: /note= "Xaa at position 59 is Glu,  
 Tyr, His, Leu, Pro, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 60  
 (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala,  
 Ser, Pro, Tyr, Asn, or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 61  
 (D) OTHER INFORMATION: /note= "Xaa at position 61 is Phe,  
 Asn, Glu, Pro, Lys, Arg, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 62  
 (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn,  
 His, Val, Arg, Pro, Thr, Asp, or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 63  
 (D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg,  
 Tyr, Trp, Lys, Ser, His, Pro, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 64  
 (D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala,  
 Asn, Pro, Ser, or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 65  
 (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val,  
 Thr, Pro, His, Leu, Phe, or Ser"



- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 66  
 (D) OTHER INFORMATION: /note= "Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 67  
 (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 68  
 (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 69  
 (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 70  
 (D) OTHER INFORMATION: /note= "Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 71  
 (D) OTHER INFORMATION: /note= "Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 72  
 (D) OTHER INFORMATION: /note= "Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 73  
 (D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 74  
 (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 75  
 (D) OTHER INFORMATION: /note= "Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 76  
 (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser,

Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 77
- (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 78
- (D) OTHER INFORMATION: /note= "Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 79
- (D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 80
- (D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 81
- (D) OTHER INFORMATION: /note= "Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 82
- (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe, Ile, Met, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 83
- (D) OTHER INFORMATION: /note= "Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 84
- (D) OTHER INFORMATION: /note= "Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 85
- (D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu, Asn, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 86
- (D) OTHER INFORMATION: /note= "Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 87

- (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu, Ser, Trp, or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 88  
(D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala, Lys, Arg, Val, or Trp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 89  
(D) OTHER INFORMATION: /note= "Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn, or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 90  
(D) OTHER INFORMATION: /note= "Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or Met"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 91  
(D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or His"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 92  
(D) OTHER INFORMATION: /note= "Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly, Ile, or Leu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 93  
(D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 94  
(D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 95  
(D) OTHER INFORMATION: /note= "Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 96  
(D) OTHER INFORMATION: /note= "Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 97  
(D) OTHER INFORMATION: /note= "Xaa at position 97 is Ile, Val, Lys, Ala, or Asn"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site

- (B) LOCATION: 98
  - (D) OTHER INFORMATION: /note= "Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr, or Pro"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 99
  - (D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 100
  - (D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 101
  - (D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 102
  - (D) OTHER INFORMATION: /note= "Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 103
  - (D) OTHER INFORMATION: /note= "Xaa at position 103 is Asp, or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 104
  - (D) OTHER INFORMATION: /note= "Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala, Phe, or Gly"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 105
  - (D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 106
  - (D) OTHER INFORMATION: /note= "Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or Pro"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 108
  - (D) OTHER INFORMATION: /note= "Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala, or Pro"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 109

(D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg,  
Thr, Pro, Glu, Tyr, Leu, Ser, or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 110

(D) OTHER INFORMATION: /note= "Xaa at position 110 is Lys,  
Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser,  
or Trp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 111

(D) OTHER INFORMATION: /note= "Xaa at position 111 is Leu,  
Ile, Arg, Asp, or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 112

(D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr,  
Val, Gln, Tyr, Glu, His, Ser, or Phe"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 113

(D) OTHER INFORMATION: /note= "Xaa at position 113 is Phe,  
Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val,  
or Asn"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 114

(D) OTHER INFORMATION: /note= "Xaa at position 114 is Tyr,  
Cys, His, Ser, Trp, Arg, or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 115

(D) OTHER INFORMATION: /note= "Xaa at position 115 is  
Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or  
Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 116

(D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys,  
Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser,  
Asn, His, Ala, Tyr, Phe, Glu, or Ile"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 117

(D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr,  
Ser, Asn, Ile, Trp, Lys, or Pro"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 118

(D) OTHER INFORMATION: /note= "Xaa at position 118 is Leu,  
Ser, Pro, Ala, Glu, Cys, Asp, or Tyr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 119

(D) OTHER INFORMATION: /note= "Xaa at position 119 is Glu,  
Ser, Lys, Pro, Leu, Thr, Tyr, or Arg"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 120
- (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 121
- (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 122
- (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 123
- (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys
1				5					10					15	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25					30		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35					40					45			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		50				55					60				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65					70				75					80	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			85					90					95		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Xaa
			100					105					110		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Gln	Thr	Thr	Leu
		115					120					125			
Ser	Leu	Ala	Ile	Phe											
		130													

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 1  
 (D) OTHER INFORMATION: /note= "Met- may or may not precede  
 the amino acid in position 1"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 17  
 (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser,  
 Gly, Asp, Met, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 18  
 (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn,  
 His, Leu, Ile, Phe, Arg, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 19  
 (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met,  
 Phe, Ile, Arg, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 20  
 (D) OTHER INFORMATION: /note= "Xaa at position 20 is Ile  
 or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 21  
 (D) OTHER INFORMATION: /note; "Xaa at position 21 is Asp  
 or Glu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 23  
 (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile,  
 Val, Ala, Leu, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 24  
 (D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile,  
 Val, Phe, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 25  
 (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr,  
 His, Gly, Gln, Arg, Pro, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 26  
 (D) OTHER INFORMATION: /note= "Xaa at position 26 is His,  
 Phe, Gly, Arg, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 28  
 (D) OTHER INFORMATION: /note= "Xaa at position 28 is Lys,  
 Leu, Gln, Gly, Pro, or Val"
- (ix) FEATURE:



- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 29
  - (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln, Asn, Leu, Arg, or Val"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 30
  - (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro, His, Thr, Gly, or Gln"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 31
  - (D) OTHER INFORMATION: /note= "Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 32
  - (D) OTHER INFORMATION: /note= "Xaa at position 32 Leu, Arg, Gln, Asn, Gly, Ala, or Glu"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 33
  - (D) OTHER INFORMATION: /note= "Xaa at position 33 is Pro, Leu, Gln, Ala, or Glu"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 34
  - (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 35
  - (D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu, Ala, Asn, Pro, Gln, or Val"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 36
  - (D) OTHER INFORMATION: /note= "Xaa at position 36 is Asp or Leu"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 37
  - (D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 38
  - (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn or Ala"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 41
  - (D) OTHER INFORMATION: /note= "Xaa at position 41 is Asn, Cys, Arg, His, Met, or Pro"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 42  
 (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,  
 Asp, Ser, Cys, Ala, Asn, Ile, Leu, Met, Tyr, Val,  
 or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 44  
 (D) OTHER INFORMATION: /note="Xaa at position 44 is Asp or Glu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 45  
 (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,  
 Val, Met, Leu, Thr, Lys, Ala, Asn, Glu, Ser, or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 46  
 (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp,  
 Phe, Ser, Thr, Cys, Ala, Asn, Gln, Glu, His, Ile, Lys,  
 Tyr, Val, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 47  
 (D) OTHER INFORMATION: /note= "Xaa at position 47 is Ile, Val,  
 or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 49  
 (D) OTHER INFORMATION: /note= "Xaa at position 49 is Met,  
 Asn, or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 50  
 (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu,  
 Thr, Ala, Asn, Ser, or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 51  
 (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn,  
 Arg, Met, Pro, Ser, Thr, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 52  
 (D) OTHER INFORMATION: /note= "Xaa at position 52 is Asn  
 or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 53  
 (D) OTHER INFORMATION: /note= "Xaa at position 53 is Leu,  
 Met, or Phe"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 54  
 (D) OTHER INFORMATION: /note= "Xaa at position 54 is Arg  
 Ala, or Ser"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 55  
 (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg, Thr, Val, Leu, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 56  
 (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Ala, Arg, Asn, Glu, His, Leu, Thr, Val, or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 59  
 (D) OTHER INFORMATION: /note= "Xaa at position 59 is Glu, Tyr, His, Leu, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 60  
 (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala, Ser, Asn, or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 61  
 (D) OTHER INFORMATION: /note= "Xaa at position 61 is Phe or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 62  
 (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn, Val, Pro, Thr, or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 63  
 (D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg, Tyr, Lys, Ser, His, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 64  
 (D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala or Asn"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 65  
 (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val, Thr, Leu, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 66  
 (D) OTHER INFORMATION: /note= "Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 67  
 (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser,

Phe, Val, Gly, Asn, Ile, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 68
- (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu, Val, Ile, Phe, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 69
- (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 70
- (D) OTHER INFORMATION: /note= "Xaa at position 70 is Asn or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 71
- (D) OTHER INFORMATION: /note= "Xaa at position 71 is Ala, Met, Pro, Arg, Glu, Thr, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 72
- (D) OTHER INFORMATION: /note= "Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 73
- (D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, Arg, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 74
- (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ile or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 75
- (D) OTHER INFORMATION: /note= "Xaa at position 75 is Glu, Gly, Asp, Ser, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 76
- (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser, Val, Ala, Asn, Glu, Pro, Gly, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 77
- (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile, Ser, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 79
- (D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys,

Thr, Asn, Met, Arg, Ile, Gly, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 80
- (D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn, Val, Gly, Thr, Leu, Glu, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 81
- (D) OTHER INFORMATION: /note= "Xaa at position 81 is Leu or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 82
- (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu, Gln, Trp, Arg, Asp, Ala, Asn, Glu, His, Met, Phe, Ser, Thr, Tyr, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 83
- (D) OTHER INFORMATION: /note= "Xaa at position 83 is Pro, Ala, Thr, Trp, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 85
- (D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 87
- (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 88
- (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala, Arg, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 89
- (D) OTHER INFORMATION: /note= "Xaa at position 89 is Thr, Asp, Glu, His, Asn, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 90
- (D) OTHER INFORMATION: /note= "Xaa at position 90 is Ala, Asp, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 91
- (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 92

(D) OTHER INFORMATION: /note= "Xaa at position 92 is Pro  
or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 93

(D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr,  
Asp, Ser, Pro, Ala, Leu, or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 95

(D) OTHER INFORMATION: /note= "Xaa at position 95 is His,  
Pro, Arg, Val, Leu, Gly, Asn, Ile, Phe, Ser,  
or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 96

(D) OTHER INFORMATION: /note= "Xaa at position 96 is Pro  
or Tyr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 97

(D) OTHER INFORMATION: /note= "Xaa at position 97 is Ile,  
Val, or Ala"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 98

(D) OTHER INFORMATION: /note= "Xaa at position 98 is His,  
Ile, Asn, Leu, Asp, Ala, Thr, Arg, Gln, Glu,  
Lys, Met, Ser, Tyr, Val, or Pro"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 99

(D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile,  
Leu, Val, or Phe"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 100

(D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys,  
Leu, His, Arg, Ile, Gln, Pro, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 101

(D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp,  
Pro, Met, Lys, His, Thr, Val, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 102

(D) OTHER INFORMATION: /note= "Xaa at position 102 is Gly,  
Glu, Lys, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 104

(D) OTHER INFORMATION: /note= "Xaa at position 104 is Trp,  
Val, Tyr, Met, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 105
  - (D) OTHER INFORMATION: /note= "Xaa at position 105 is  
Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys,  
Ile, Asp or His"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 106
  - (D) OTHER INFORMATION: /note= "Xaa at position 106 is Glu,  
Ser, Ala, or Gly"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 108
  - (D) OTHER INFORMATION: /note= "Xaa at position 108 is Arg,  
Ala, Gln, Ser, or Lys"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 109
  - (D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg,  
Thr, Glu, Leu, Ser, or Gly"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 112
  - (D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr,  
Val, Gln, Glu, His, or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 114
  - (D) OTHER INFORMATION: /note= "Xaa at position 114 is Tyr  
or Trp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 115
  - (D) OTHER INFORMATION: /note= "Xaa at position 115 is Leu  
or Ala"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 116
  - (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys,  
Thr, Met, Val, Trp, Ser, Leu, Ala, Asn, Gln, His, Phe,  
Tyr, or Ile"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 117
  - (D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr,  
Ser, or Asn"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 119
  - (D) OTHER INFORMATION: /note= "Xaa at position 119 is  
Glu, Ser, Pro, Leu, Thr, or Tyr"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 120
  - (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn,  
Pro, Leu, His, Val, or Gln"



## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 121
- (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 122
- (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 123
- (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys	1	5	10	15
Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	20	25	30	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Leu	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Leu	35	40	45	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	50	55	60	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	65	70	75	80
Xaa	Xaa	Xaa	Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Xaa	85	90	95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Lys	Leu	Xaa	100	105	110	
Phe	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Gln	Thr	Thr	Leu	115	120	125	
Ser	Leu	Ala	Ile	Phe												130			

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 17  
 (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser,  
 Gly, Asp, Met, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 18  
 (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn,  
 His, or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 19  
 (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met  
 or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 21  
 (D) OTHER INFORMATION: /note= "Xaa at position 21 is Asp  
 or Glu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 23  
 (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile,  
 Ala, Leu, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 24  
 (D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile,  
 Val, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 25  
 (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr,  
 His, Gln, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 26  
 (D) OTHER INFORMATION: /note= "Xaa at position 26 is His  
 or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 29  
 (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln,  
 Asn, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 30  
 (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro,  
 Gly, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 31  
 (D) OTHER INFORMATION: /note= "Xaa at position 31 is Pro,  
 Asp, Gly, or Gln"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 32  
 (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu,  
 Arg, Gln, Asn, Gly, Ala, or Glu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 33  
 (D) OTHER INFORMATION: /note= "Xaa at position 33 is Pro  
 or Glu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 34  
 (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu,  
 Val, Gly, Ser, Lys, Ala, Arg, Gln, Glu, Ile, Phe  
 Thr, or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 35  
 (D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu,  
 Ala, Asn, Pro, Gln, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 37  
 (D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe,  
 Ser, Pro, or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 38  
 (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn  
 or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 42  
 (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,  
 Asp, Ser, Cys, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 44  
 (D) OTHER INFORMATION: /note= "Xaa at position 44 is Asp  
 or Glu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 45  
 (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,  
 Val, Met, Leu, Thr, Ala, Asn, Glu, Ser, or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 46  
 (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp,  
 Phe, Ser, Thr, Ala, Asn, Gln, Glu, His, Ile, Lys,  
 Tyr, Val, or Cys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 50  
 (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu,

Ala, Asn, Ser, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 51
- (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 54
- (D) OTHER INFORMATION: /note= "Xaa at position 54 is Arg or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 55
- (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg, Thr, Val, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 56
- (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro, Gly, Ser, Gln, Ala, Arg, Asn, Glu, Leu, Thr, Val, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 60
- (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 62
- (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn, Pro, Thr, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 63
- (D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 64
- (D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 65
- (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 66
- (D) OTHER INFORMATION: /note= "Xaa at position 66 is Lys or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 67

- (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser  
Phe or His"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 68  
(D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,  
Ile, Phe, or His"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 69  
(D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln,  
Ala, Pro, Thr, Glu, Arg, or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 71  
(D) OTHER INFORMATION: /note= "Xaa at position 71 is Ala,  
Pro, or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 72  
(D) OTHER INFORMATION: /note= "Xaa at position 72 is Ser,  
Glu, Arg, or Asp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 73  
(D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala  
or Leu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 76  
(D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser,  
Val, Ala, Asn, Glu, Pro, or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 77  
(D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile  
or Leu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 79  
(D) OTHER INFORMATION: /note= "Xaa at position 79 is  
Lys, Thr, Asn, Met, Arg, Ile, Gly, or Asp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 80  
(D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn,  
Gly, Glu, or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 82  
(D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu,  
Gln, Trp, Arg, Asp, Ala, Asn, Glu, His, Ile, Met,  
Phe, Ser, Thr, Tyr, or Val"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site

- (B) LOCATION: 83
  - (D) OTHER INFORMATION: /note= "Xaa at position 83 is Pro or Thr"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 85
  - (D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu or Val"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 87
  - (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 88
  - (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala or Trp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 91
  - (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala or Pro"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 93
  - (D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr, Asp, Ser, Pro, Ala, Leu, or Arg"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 95
  - (D) OTHER INFORMATION: /note= "Xaa at position 95 is His, Pro, Arg, Val, Leu, Gly, Asn, Phe, Ser, or Thr"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 96
  - (D) OTHER INFORMATION: /note= "Xaa at position 96 is Pro or Tyr"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 97
  - (D) OTHER INFORMATION: /note= "Xaa at position 97 is Ile or Val"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 98
  - (D) OTHER INFORMATION: /note= "Xaa at position 98 is His, Ile, Asn, Leu, Ala, Thr, Arg, Gln, Lys, Met, Ser, Tyr, Val, or Pro"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 99
  - (D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile, Leu, or Val"
- (ix) FEATURE:

- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 100
  - (D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys, Arg, Ile, Gln, Pro, or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 101
  - (D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Pro, Asn, Ile, Leu, or Tyr"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 104
  - (D) OTHER INFORMATION: /note= "Xaa at position 104 is Trp or Leu"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 105
  - (D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn, Pro, Ala, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 106
  - (D) OTHER INFORMATION: /note= "Xaa at position 106 is Glu or Gly"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 109
  - (D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg, Thr, Glu, Leu, or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 112
  - (D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr, Val, or Gln"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 114
  - (D) OTHER INFORMATION: /note= "Xaa at position 114 is Tyr or Trp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 115
  - (D) OTHER INFORMATION: /note= "Xaa at position 115 is Leu or Ala"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 116
  - (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys, Thr, Val, Trp, Ser, Ala, His, Met, Phe, Tyr, or Ile"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 117
  - (D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr or Ser"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 120
- (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn, Pro, Leu, His, Val, or Gln"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 121
- (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Asp, or Gly"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 122
- (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 123
- (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys
1				5					10					15	
Xaa	Xaa	Xaa	Ile	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Leu	Lys	Xaa	Xaa	Xaa	Xaa
			20					25					30		
Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Asn	Leu	Asn	Xaa	Glu	Xaa	Xaa	Xaa	Ile	Leu
			35				40					45			
Met	Xaa	Xaa	Asn	Leu	Xaa	Xaa	Xaa	Asn	Leu	Glu	Xaa	Phe	Xaa	Xaa	Xaa
			50				55				60				
Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Ile	Glu	Xaa	Xaa	Leu	Xaa	Xaa
65					70				75					80	
Leu	Xaa	Xaa	Cys	Xaa	Pro	Xaa	Xaa	Thr	Ala	Xaa	Pro	Xaa	Arg	Xaa	Xaa
			85						90					95	
Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Asp	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Lys	Leu	Xaa
			100				105						110		
Phe	Xaa	Xaa	Xaa	Xaa	Leu	Glu	Xaa	Xaa	Xaa	Gln	Gln	Thr	Thr	Leu	
			115				120				125				
Ser	Leu	Ala	Ile	Phe											
			130												

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:



- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser, Gly, Asp, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn, His, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile, Ala, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr, His, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 26
- (D) OTHER INFORMATION: /note= "Xaa at position 26 is His or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu, Arg, Asn, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 34
- (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu, Val, Ser, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu, Ala, Asn, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 38
- (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 42
- (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly, Asp, Ser, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 45
- (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln, Val, Met, Leu, Ala, Asn, Glu, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 46
- (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp, Phe, Ser, Gln, Glu, His, Val, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 50
- (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu, Asn, Ser, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 51
- (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn, Arg, Pro, Thr, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 55
- (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 56
- (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro, Gly, Ser, Ala, Asn, Val, Leu, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 62
- (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn, Pro, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 64
- (D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 65
- (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 67
  - (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser or Phe"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 68
  - (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu or Phe"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 69
  - (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln, Ala, Glu, or Arg"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 76
  - (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser, Val, Asn, Pro, or Gly"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 77
  - (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile or Leu"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 79
  - (D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys, Asn, Met, Arg, Ile, or Gly"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 80
  - (D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn, Gly, Glu, or Arg"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 82
  - (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu, Gln, Trp, Arg, Asp, Asn, Glu, His, Met, Phe, Ser, Thr, Tyr, or Val"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 87
  - (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 88
  - (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala or Trp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 91
  - (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala or Pro"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 93  
 (D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr,  
 Asp, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 95  
 (D) OTHER INFORMATION: /note= "Xaa at position 95 is His,  
 Pro, Arg, Val, Gly, Asn, Ser, or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 98  
 (D) OTHER INFORMATION: /note= "Xaa at position 98 is His,  
 Ile, Asn, Ala, Thr, Arg, Gln, Glu, Lys, Met, Ser,  
 Tyr, Val, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 99  
 (D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile  
 or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 100  
 (D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys  
 or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 101  
 (D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp,  
 Pro, Met, Lys, Thr, His, Pro, Asn, Ile, Leu, or Tyr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 105  
 (D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn,  
 Pro, Ser, Ile, or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 108  
 (D) OTHER INFORMATION: /note= "Xaa at position 108 is Arg, Ala,  
 or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 109  
 (D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg,  
 Thr, Glu, Leu, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 112  
 (D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr  
 or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 116  
 (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys,  
 Val, Trp, Ala, His, Phe, Tyr, or Ile"

(ix) FEATURE:

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(A) NAME/KEY: Modified-site
(B) LOCATION: 117
(D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr
                        or Ser"
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(ix) FEATURE:

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(A) NAME/KEY: Modified-site
(B) LOCATION: 120
(D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn,
    Pro, Leu, His, Val, or Gln"

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(ix) FEATURE:

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(A) NAME/KEY: Modified-site
(B) LOCATION: 121
(D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala,
    Ser, Ile, Pro, or Asp"      (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 122
(D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln,
    Met, Trp, Phe, Pro, His, Ile, or Tyr"
```

(ix) FEATURE:

```
(A) NAME/KEY: Modified-site
(B) LOCATION: 123
(D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala,
    Met, Glu, Ser, or Leu"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

[illegible]

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 1  
 (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may  
 not precede the amino acid in position 1"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 3  
 (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser,  
 Lys, Gly, Asp, Met, Gln, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 4  
 (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn,  
 His, Leu, Ile, Phe, Arg, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 5  
 (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met,  
 Phe, Ile, Arg, Gly, Ala, or Cys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: /note= "Xaa at position 6 is Ile,  
 Cys, Gln, Glu, Arg, Pro, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: /note= "Xaa at position 7 is Asp,  
 Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser,  
 or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: /note= "Xaa at position 8 is Glu,  
 Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val,  
 or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 9  
 (D) OTHER INFORMATION: /note= "Xaa at position 9 is  
 Ile, Val, Ala, Leu, Gly, Trp, Lys, Phe, Ser  
 or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: /note= "Xaa at position 10 is Ile,  
 Gly, Val, Arg, Ser, Phe, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 11  
 (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr,  
 His, Gly, Gln, Arg, Pro, or Ala"
- (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "Xaa at position 12 is His, Thr, Phe, Gly, Arg, Ala, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /note= "Xaa at position 13 is Leu, Gly, Arg, Thr, Ser, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /note= "Xaa at position 14 is Lys, Arg, Leu, Gln, Gly, Pro, Val, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln, Asn, Leu, Pro, Arg, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "Xaa at position 17 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /note= "Xaa at position 19 is Pro, Leu, Gln, Ala, Thr, or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe, Ile, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu, Ala, Gly, Asn, Pro, Gln, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 22
- (D) OTHER INFORMATION: /note= "Xaa at position 22 is Asp, Leu, or Val"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 23  
 (D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe,  
 Ser, Pro, Trp, or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 24  
 (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn  
 or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 26  
 (D) OTHER INFORMATION: /note= "Xaa at position 26 is Leu,  
 Trp, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 27  
 (D) OTHER INFORMATION: /note= "Xaa at position 27 is Asn,  
 Cys, Arg, Leu, His, Met, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 28  
 (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly,  
 Asp, Ser, Cys, Ala, Lys, Asn, Thr, Leu, Val, Glu,  
 Phe, Tyr, Ile, or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 29  
 (D) OTHER INFORMATION: /note= "Xaa at position 29 is Glu,  
 Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr,  
 Gly, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 30  
 (D) OTHER INFORMATION: /note= "Xaa at position 30 is Asp,  
 Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln,  
 Ala, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 31  
 (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln,  
 Pro, Phe, Val, Met, Leu, Thr, Lys, Asp, Asn, Arg,  
 Ser, Ala, Ile, Glu, His, or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 32  
 (D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp,  
 Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala,  
 Tyr, Ile, Val, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 33  
 (D) OTHER INFORMATION: /note= "Xaa at position 33 is Ile,  
 Gly, Val, Ser, Arg, Pro, or His"
- (ix) FEATURE:



- (A) NAME/KEY: Modified-site
- (B) LOCATION: 34
- (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val, or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION: /note= "Xaa at position 35 is Met, Arg, Ala, Gly, Pro, Asn, His, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 36
- (D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe, Met, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn, Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 38
- (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn, His, Arg, Leu, Gly, Ser, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 39
- (D) OTHER INFORMATION: /note= "Xaa at position 39 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 40
- (D) OTHER INFORMATION: /note= "Xaa at position 40 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 41
- (D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg, Thr, Val, Ser, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 42
- (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr, Phe, Leu, Val, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 43
- (D) OTHER INFORMATION: /note= "Xaa at position 43 is Asn or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 44

- (D) OTHER INFORMATION: /note= "Xaa at position 44 is Leu, Ser, Asp, Arg, Gln, Val, or Cys"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 45  
(D) OTHER INFORMATION: /note= "Xaa at position 45 is Glu, Tyr, His, Leu, Pro, or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 46  
(D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala, Ser, Pro, Tyr, Asn, or Thr"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 47  
(D) OTHER INFORMATION: /note= "Xaa at position 47 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 48  
(D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn, His, Val, Arg, Pro, Thr, Asp, or Ile"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 49  
(D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or Val"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 50  
(D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala, Asn, Pro, Ser, or Lys"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 51  
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Val, Thr, Pro, His, Leu, Phe, or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 52  
(D) OTHER INFORMATION: /note= "Xaa at position 52 is Lys, Ile, Arg, Val, Asn, Glu, or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 53  
(D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro, or His"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 54  
(D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 55

- (D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 56  
(D) OTHER INFORMATION: /note= "Xaa at position 56 is Asn, Leu, Val, Trp, Pro, or Ala"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 57  
(D) OTHER INFORMATION: /note= "Xaa at position 57 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 58  
(D) OTHER INFORMATION: /note= "Xaa at position 58 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 59  
(D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 60  
(D) OTHER INFORMATION: /note= "Xaa at position 60 is Ile, Met, Thr, Pro, Arg, Gly, Ala"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 61  
(D) OTHER INFORMATION: /note= "Xaa at position 61 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 62  
(D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 63  
(D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile, Ser, Arg, Thr, or Leu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 64  
(D) OTHER INFORMATION: /note= "Xaa at position 64 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 65  
(D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys, Thr, Gly, Asn, Met, Arg, Ile, or Asp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site

- (B) LOCATION: 66  
(D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn,  
Trp, Val, Gly, Thr, Leu, Glu, or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 67  
(D) OTHER INFORMATION: /note= "Xaa at position 67 is Leu,  
Gln, Gly, Ala, Trp, Arg, Val, or Lys"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 68  
(D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,  
Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala,  
Tyr, Phe, Ile, Met, or Val"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 69  
(D) OTHER INFORMATION: /note= "Xaa at position 69 is Pro,  
Ala, Thr, Trp, Arg, or Met"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 70  
(D) OTHER INFORMATION: /note= "Xaa at position 70 is Cys,  
Glu, Gly, Arg, Met, or Val"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 71  
(D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu,  
Asn, Val, or Gln"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 72  
(D) OTHER INFORMATION: /note= "Xaa at position 72 is Pro,  
Cys, Arg, Ala, or Lys"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 73  
(D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu,  
Ser, Trp, or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 74  
(D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala,  
Lys, Arg, Val, or Trp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 75  
(D) OTHER INFORMATION: /note= "Xaa at position 75 is Thr,  
Asp, Cys, Leu, Val, Glu, His, Asn, or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 76  
(D) OTHER INFORMATION: /note= "Xaa at position 76 is Ala,  
Pro, Ser, Thr, Gly, Asp, Ile, or Met"
- (ix) FEATURE:

- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 77
  - (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or His"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 78
  - (D) OTHER INFORMATION: /note= "Xaa at position 78 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly, Ile, or Leu"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 79
  - (D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or Arg"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 80
  - (D) OTHER INFORMATION: /note= "Xaa at position 80 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 81
  - (D) OTHER INFORMATION: /note= "Xaa at position 81 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 82
  - (D) OTHER INFORMATION: /note= "Xaa at position 82 is Pro, Lys, Tyr, Gly, Ile, or Thr"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 83
  - (D) OTHER INFORMATION: /note= "Xaa at position 83 is Ile, Val, Lys, Ala, or Asn"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 84
  - (D) OTHER INFORMATION: /note= "Xaa at position 84 is His, Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr, or Pro"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 85
  - (D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 86
  - (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 87
  - (D) OTHER INFORMATION: /note= "Xaa at position 87 is

Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn,  
Ser, Ala, Gly, Ile, Leu, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 88
- (D) OTHER INFORMATION: /note= "Xaa at position 88 Gly,  
Leu, Glu, Lys, Ser, Tyr, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 89
- (D) OTHER INFORMATION: /note= "Xaa at position 89 is Asp  
or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 90
- (D) OTHER INFORMATION: /note= "Xaa at position 90 is  
Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys,  
Ala, Phe, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 91
- (D) OTHER INFORMATION: /note= "Xaa at position 91 is  
Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys,  
Ile, Asp, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 92
- (D) OTHER INFORMATION: /note= "Xaa at position 92 is Glu,  
Ser, Ala, Lys, Thr, Ile, Gly, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 94
- (D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg,  
Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 95
- (D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg,  
Thr, Pro, Glu, Tyr, Leu, Ser, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 96
- (D) OTHER INFORMATION: /note= "Xaa at position 96 is Lys,  
Asn, Thr, Leu, Gln, Arg, His, Glu, Ser, Ala,  
or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 97
- (D) OTHER INFORMATION: /note= "Xaa at position 97 is Leu,  
Ile, Arg, Asp, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 98
- (D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr,  
Val, Gln, Tyr, Glu, His, Ser, or Phe"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 99  
 (D) OTHER INFORMATION: /note= "Xaa at position 99 is Phe,  
 Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile,  
 Val, or Asn"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 100  
 (D) OTHER INFORMATION: /note= "Xaa at position 100 is Tyr,  
 Cys, His, Ser, Trp, Arg, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 101  
 (D) OTHER INFORMATION: /note= "Xaa at position 101 is Leu,  
 Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 102  
 (D) OTHER INFORMATION: /note= "Xaa at position 102 is  
 Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp,  
 Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 103  
 (D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr,  
 Ser, Asn, Ile, Trp, Lys, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 104  
 (D) OTHER INFORMATION: /note= "Xaa at position 104 is Leu,  
 Ser, Pro, Ala, Glu, Cys, Asp, or Tyr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 105  
 (D) OTHER INFORMATION: /note= "Xaa at position 105 is Glu,  
 Ser, Lys, Pro, Leu, Thr, Tyr, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 106  
 (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn,  
 Ala, Pro, Leu, His, Val or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 107  
 (D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala,  
 Ser, Ile, Asn, Pro, Lys, Asp, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 108  
 (D) OTHER INFORMATION: /note= "Xaa at position 108 is  
 Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr,  
 or Cys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 109

(D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala,  
Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

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Asn Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1          5          10          15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20          25          30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35          40          45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50          55          60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65          70          75          80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa
85          90          95
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln
100          105          110

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(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may  
not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser,  
Gly, Asp, Met, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn,  
His, Leu, Ile, Phe, Arg, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met,  
Phe, Ile, Arg, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "Xaa at position 6 is Ile or  
Pro"



- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: /note= "Xaa at position 7 is Asp or Glu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 9  
 (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile, Val, Ala, Leu, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: /note= "Xaa at position 10 is Ile, Val, Phe, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 11  
 (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr, His, Gly, Gln, Arg, Pro, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 12  
 (D) OTHER INFORMATION: /note= "Xaa at position 12 is His, Phe, Gly, Arg, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 14  
 (D) OTHER INFORMATION: /note= "Xaa at position 14 is Lys, Leu, Gln, Gly, Pro, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 15  
 (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln, Asn, Leu, Arg, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 16  
 (D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro, His, Thr, Gly, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 17  
 (D) OTHER INFORMATION: /note= "Xaa at position 17 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 18  
 (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu, Arg, Gln, Asn, Gly, Ala or Glu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 19  
 (D) OTHER INFORMATION: /note= "Xaa at poisiton 19 is Pro, Leu, Gln, Ala, or Glu"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 20  
 (D) OTHER INFORMATION: /note= "Xaa at positon 20 is Leu, Val, Gly, Ser, Lys, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 21  
 (D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu, Ala, Asn, Pro, Gln, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 22  
 (D) OTHER INFORMATION: /note= "Xaa at position 22 is Asp or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 23  
 (D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe, Ser, Pro, Trp, or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 24  
 (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 27  
 (D) OTHER INFORMATION: /note= "Xaa at position 27 is Asn, Cys, Arg, His, Met, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 28  
 (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly, Asp, Ser, Cys, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 30  
 (C) OTHER INFORMATION: /note= "Xaa at position 30 is Asp or Glu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 31  
 (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln, Val, Met, Leu, Thr, Lys, Ala, Asn, Glu, Ser, or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 32  
 (D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp, Phe, Ser, Thr, Cys, Ala, Asn, Gln, Glu, His, Ile, Lys, Tyr, Val, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 33  
 (D) OTHER INFORMATION: /note= "Xaa at position 33 is Ile,

Val, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION: /note= "Xaa at position 35 is Met, Asn, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 36
- (D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu, Thr, Ala, Asn, Ser, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn, Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 38
- (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 39
- (D) OTHER INFORMATION: /note= "Xaa at position 39 is Leu, Met, or Phe"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 40
- (D) OTHER INFORMATION: /note= "Xaa at position 40 is Arg, Ala, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 41
- (D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg, Thr, Val, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 42
- (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro, Gly, Cys, Ser, Gln, Ala, Arg, Asn, Glu, His, Leu, Thr, Val, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 45
- (D) OTHER INFORMATION: /note= "Xaa at position 45 is Glu, Tyr, His, Leu, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 46
- (D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala, Ser, Asn, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 47

(D) OTHER INFORMATION: /note= "Xaa at position 47 is Phe  
or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 48  
(D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn,  
Val, Pro, Thr, or Ile"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 49  
(D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg,  
Tyr, Lys, Ser, His, or Val"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 50  
(D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala  
or Asn"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 51  
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Val,  
Thr, Leu, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 52  
(D) OTHER INFORMATION: /note= "Xaa at position 52 is Lys,  
Ile, Arg, Val, Asn, Glu, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 53  
(D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser,  
Phe, Val, Gly, Asn, Ile, or His"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 54  
(D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu,  
Val, Ile, Phe, or His"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 55  
(D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln,  
Ala, Pro, Thr, Glu, Arg, or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 56  
(D) OTHER INFORMATION: /note= "Xaa at position 56 is Asn  
or Pro"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 57  
(D) OTHER INFORMATION: /note= "Xaa at position 57 is Ala,  
Met, Pro, Arg, Glu, Thr, or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 58

(D) OTHER INFORMATION: /note= "Xaa at position 58 is Ser,  
Glu, Met, Ala, His, Asn, Arg, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 59

(D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala,  
Glu, Asp, Leu, Ser, Gly, Thr, Arg, or Pro"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 60

(D) OTHER INFORMATION: /note= "Xaa at position 60 is Ile  
or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 61

(D) OTHER INFORMATION: /note= "Xaa at position 61 is Glu,  
Gly, Asp, Ser, or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 62

(D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,  
Val, Ala, Asn, Glu, Pro, Gly, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 63

(D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile,  
Ser, or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 65

(D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,  
Thr, Gly, Asn, Met, Arg, Ile, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 66

(D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn,  
Val, Gly, Thr, Leu, Glu, or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 67

(D) OTHER INFORMATION: /note= "Xaa at position 67 is Leu  
or Val"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 68

(D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,  
Gln, Trp, Arg, Asp, Ala, Asn, Glu, His, Met, Phe,  
Ser, Thr, Tyr, or Val"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 69

(D) OTHER INFORMATION: /note= "Xaa at position 69 is Pro,  
Ala, Thr, Trp, or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

- (B) LOCATION: 71
  - (D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu or Val"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 73
  - (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 74
  - (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala, Arg, or Trp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 75
  - (D) OTHER INFORMATION: /note= "Xaa at position 75 is Thr, Asp, Glu, His, Asn, or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 76
  - (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ala, Asp, or Met"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 77
  - (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala, Pro, Ser, Thr, Phe, Leu, or Asp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 78
  - (D) OTHER INFORMATION: /note= "Xaa at position 78 is Pro or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 79
  - (D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr, Asp, Ser, Pro, Ala, Leu, or Arg"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 81
  - (D) OTHER INFORMATION: /note= "Xaa at position 81 is His, Pro, Arg, Val, Leu, Gly, Asn, Ile, Phe, Ser, or Thr"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 82
  - (D) OTHER INFORMATION: /note= "Xaa at position 82 is Pro or Tyr"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 83
  - (D) OTHER INFORMATION: /note= "Xaa at position 83 is Ile, Val, or Ala"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site

- (B) LOCATION: 84
  - (D) OTHER INFORMATION: /note= "Xaa at position 84 is His, Ile, Asn, Leu, Asp, Ala, Thr, Arg, Gln, Glu, Lys, Met, Ser, Tyr, Val, or Pro"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 85
  - (D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile, Leu, Val, or Phe"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 86
  - (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys, Leu, His, Arg, Ile, Gln, Pro, or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 87
  - (D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp, Pro, Met, Lys, His, Thr, Val, Asn, Ile, Leu, or Tyr"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 88
  - (D) OTHER INFORMATION: /note= "Xaa at position 88 is Gly, Glu, Lys, or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 90
  - (D) OTHER INFORMATION: /note= "Xaa at position 90 is Trp, Val, Tyr, Met, or Leu"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 91
  - (D) OTHER INFORMATION: /note= "Xaa at position 91 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 92
  - (D) OTHER INFORMATION: /note= "Xaa at position 92 is Glu, Ser, Ala, or Gly"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 94
  - (D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg, Ala, Gln, Ser, or Lys"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 95
  - (D) OTHER INFORMATION: /note= "Xaa at position 95 Arg, Thr, Glu, Leu, Ser, or Gly"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 98
  - (D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr, Val, Gln, Glu, His, or Ser"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 100  
 (D) OTHER INFORMATION: /note= "Xaa at position 100 is Tyr or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 101  
 (D) OTHER INFORMATION: /note= "Xaa at position 101 is Leu or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 102  
 (D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys, Thr, Met, Val, Trp, Ser, Leu, Ala, Asn, Gln, His, Phe, Tyr, or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 103  
 (D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr, Ser, or Asn"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 105  
 (D) OTHER INFORMATION: /note= "Xaa at position 105 is Glu, Ser, Pro, Leu, Thr, or Tyr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 106  
 (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn, Pro, Leu, His, Val, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 107  
 (D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 108  
 (D) OTHER INFORMATION: /note= "Xaa at position 108 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 109  
 (D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Cys | Xaa | Xaa | Xaa | Xaa | Xaa | Glu | Xaa | Xaa | Xaa | Xaa | Leu | Xaa | Xaa | Xaa |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Asn | Leu | Xaa | Xaa | Glu | Xaa | Xaa | Xaa |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Xaa | Leu | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Asn | Leu | Xaa | Xaa | Xaa | Xaa |



	35		40		45	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	50		55		60	
Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa
65			70		75	
Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa
		85		90		
Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa
						95
Leu	Xaa	Phe	Xaa	Xaa	Xaa	Xaa
	100			105		
						Gln
						110

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser, Gly, Asp, Met, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn, His, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (C) OTHER INFORMATION: /note= "Xaa at position 7 is Asp or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile, Ala, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /note= "Xaa at position 10 is Ile, Val, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

- (B) LOCATION: 11
  - (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr, His, Gln, or Ala"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 12
  - (D) OTHER INFORMATION: /note= "Xaa at position 12 is His or Ala"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 15
  - (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln, Asn, or Val"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 16
  - (D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro, Gly, or Gln"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 17
  - (D) OTHER INFORMATION: /note= "Xaa at position 17 is Pro, Asp, Gly, or Gln"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 18
  - (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu, Arg, Gln, Asn, Gly, Ala, or Glu"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 19
  - (D) OTHER INFORMATION: /note= "Xaa at position 19 is Pro or Glu"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 20
  - (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu, Val, Gly, Ser, Lys, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 21
  - (D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu, Ala, Asn, Pro, Gln, or Val"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 23
  - (D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe, Ser, Pro, or Trp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 24
  - (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn or Ala"
- (ix) FEATURE:

- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 28
  - (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly, Asp, Ser, Cys, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 30
  - (D) OTHER INFORMATION: /note= "Xaa at position 30 is Asp or Glu"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 31
  - (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln, Val, Met, Leu, Thr, Ala, Asn, Glu, Ser, or Lys"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 32
  - (D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp, Phe, Ser, Thr, Ala, Asn, Gln, Glu, His, Ile, Lys, Tyr, Val, or Cys"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 36
  - (D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu, Ala, Asn, Ser, or Asp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 37
  - (D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn, Arg, Met, Pro, Ser, Thr, or His"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 40
  - (D) OTHER INFORMATION: /note= "Xaa at position 40 is Arg or Ala"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 41
  - (D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg, Thr, Val, Leu, or Gly"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 42
  - (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro, Gly, Ser, Gln, Ala, Arg, Asn, Glu, Leu, Thr, Val, or Lys"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 46
  - (D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 48
  - (D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn, Pro, Thr, or Ile"

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 49
      (D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg
                               or Lys"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 50
      (D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala
                               or Asn"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 51
      (D) OTHER INFORMATION: /note= "Xaa at position 51 is Val
                               or Thr"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 52
      (D) OTHER INFORMATION: /note= "Xaa at position 52 is Lys
                               or Arg"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 53
      (D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser,
          Phe, or His"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 54
      (D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu,
          Ile, Phe, or His"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 55
      (D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln,
          Ala, Pro, Thr, Glu, Arg, or Gly"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 57
      (D) OTHER INFORMATION: /note= "Xaa at position 57 is Ala,
          Pro, or Arg"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 58
      (D) OTHER INFORMATION: /note= "Xaa at position 58 is Ser,
          Glu, Arg, or Asp"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 59
      (D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala
                               or Leu"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 62
      (D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,
          Val, Ala, Asn, Glu, Pro, or Gly"
```

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 63  
 (D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile  
 or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 65  
 (D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,  
 Thr, Gly, Asn, Met, Arg, Ile, or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 66  
 (D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn,  
 Gly, Glu, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 68  
 (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,  
 Gln, Trp, Arg, Asp, Ala, Asn, Glu, His, Ile, Met,  
 Phe, Ser, Thr, Tyr, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 69  
 (D) OTHER INFORMATION: /note= "Xaa at position 69 is Pro  
 or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 71  
 (D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu  
 or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 73  
 (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu  
 or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 74  
 (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala  
 or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 77  
 (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala  
 or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 79  
 (D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr,  
 Asp, Ser, Pro, Ala, Leu, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 81  
 (D) OTHER INFORMATION: /note= "Xaa at position 81 is His,

Pro, Arg, Val, Leu, Gly, Asn, Phe, Ser, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 82
- (D) OTHER INFORMATION: /note= "Xaa at position 82 is Pro or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 83
- (D) OTHER INFORMATION: /note= "Xaa at position 83 is Ile or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 84
- (D) OTHER INFORMATION: /note= "Xaa at position 84 is His, Ile, Asn, Leu, Ala, Thr, Arg, Gln, Lys, Met, Ser, Tyr, Val, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 85
- (D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile, Leu, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 86
- (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys, Arg, Ile, Gln, Pro, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 87
- (D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp, Pro, Met, Lys, His, Thr, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 90
- (D) OTHER INFORMATION: /note= "Xaa at position 90 is Trp or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 91
- (D) OTHER INFORMATION: /note= "Xaa at position 91 is Asn, Pro, Ala, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 92
- (D) OTHER INFORMATION: /note= "Xaa at position 92 is Glu or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 94
- (C) OTHER INFORMATION: /note= "Xaa at position 94 is Arg, Ala, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 95

(D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg,  
Thr, Glu, Leu, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 98

(D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr,  
Val, or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 100

(D) OTHER INFORMATION: /note= "Xaa at position 100 is Tyr  
or Trp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 101

(D) OTHER INFORMATION: /note= "Xaa at position 101 is Leu  
or Ala"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 102

(D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys,  
Thr, Val, Trp, Ser, Ala, His, Met, Phe, Tyr, or Ile"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 103

(D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr  
or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 106

(D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn,  
Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 107

(D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala,  
Ser, Ile, Asn, Pro, Asp, or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 108

(D) OTHER INFORMATION: /note= "Xaa at position 108 is Gln,  
Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 109

(D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala,  
Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asn	Cys	Xaa	Xaa	Xaa	Ile	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Leu	Lys	Xaa	Xaa
1				5				10						15	

Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Asn	Leu	Asn	Xaa	Glu	Xaa	Xaa	Xaa
				20				25						30	

Ile	Leu	Met	Xaa	Xaa	Asn	Leu	Xaa	Xaa	Xaa	Asn	Leu	Glu	Xaa	Phe	Xaa
		35					40					45			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Ile	Glu	Xaa	Xaa	Leu
	50						55				60				
Xaa	Xaa	Leu	Xaa	Xaa	Cys	Xaa	Pro	Xaa	Xaa	Thr	Ala	Xaa	Pro	Xaa	Arg
	65				70					75					80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Asp	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Lys
			85					90						95	
Leu	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Leu	Glu	Xaa	Xaa	Xaa	Xaa	Gln	Gln	
		100						105					110		

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser, Gly, Asp, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn, His, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile, Ala, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr, His, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "Xaa at position 12 is His or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln or Asn"



- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 16  
 (D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro  
 or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 18  
 (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu,  
 Arg, Asn, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 20  
 (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu,  
 Val, Ser, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 21  
 (D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu,  
 Ala, Asn, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 24  
 (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn  
 or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 28  
 (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly,  
 Asp, Ser, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 31  
 (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln,  
 Val, Met, Leu, Ala, Asn, Glu, or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 32  
 (D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp,  
 Phe, Ser, Ala, Gln, Glu, His, Val, or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 36  
 (D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu,  
 Asn, Ser, or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 37  
 (D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn,  
 Arg, Pro, Thr, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 41  
 (D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg,  
 Leu, or Gly"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 42  
 (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro,  
 Gly, Ser, Ala, Asn, Val, Leu, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 48  
 (D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn,  
 Pro, or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 50  
 (D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala  
 or Asn"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 51  
 (D) OTHER INFORMATION: /note= "Xaa at position 51 is Val  
 or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 53  
 (D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser  
 or Phe"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 54  
 (D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu  
 or Phe"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 55  
 (D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln,  
 Ala, Glu, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 62  
 (D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,  
 Val, Asn, Pro, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 63  
 (D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile  
 or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 65  
 (D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,  
 Asn, Met, Arg, Ile, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 66  
 (D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn,  
 Gly, Glu, or Arg"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 68  
 (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,  
 Gln, Trp, Arg, Asp, Asn, Glu, His, Met, Phe, Ser,  
 Thr, Tyr, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 73  
 (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu  
 or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 74  
 (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala  
 or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 77  
 (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala  
 or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 79  
 (D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr,  
 Asp, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 81  
 (D) OTHER INFORMATION: /note= "Xaa at position 81 is His,  
 Pro, Arg, Val, Gly, Asn, Ser, or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 84  
 (D) OTHER INFORMATION: /note= "Xaa at position 84 is His,  
 Ile, Asn, Ala, Thr, Arg, Gln, Glu, Lys, Met,  
 Ser, Tyr, Val, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 85  
 (D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile  
 or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 86  
 (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys  
 or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 87  
 (D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp,  
 Pro, Met, Lys, His, Pro, Asn, Ile, Leu, or Tyr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 91

(D) OTHER INFORMATION: /note= "Xaa at position 91 is Asn,  
Pro, Ser, Ile, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 94

(D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg,  
Ala, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 95

(D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg,  
Thr, Glu, Leu, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 98

(D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr  
or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 102

(D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys,  
Val, Trp, or Ile"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 103

(D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr,  
Ala, His, Phe, Tyr, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 106

(D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn,  
Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 107

(D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala,  
Ser, Ile, Pro, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 108

(D) OTHER INFORMATION: /note= "Xaa at position 108 is Gln,  
Met, Trp, Phe, Pro, His, Ile, or Tyr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 109

(D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala,  
Met, Glu, Ser, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asn	Cys	Xaa	Xaa	Met	Ile	Asp	Glu	Xaa	Ile	Xaa	Xaa	Leu	Lys	Xaa	Xaa
1				5					10					15	

Pro	Xaa	Pro	Xaa	Xaa	Asp	Phe	Xaa	Asn	Leu	Asn	Xaa	Glu	Asp	Xaa	Xaa
				20				25						30	

Ile	Leu	Met	Xaa	Xaa	Asn	Leu	Arg	Xaa	Xaa	Asn	Leu	Glu	Ala	Phe	Xaa
		35					40					45			
Arg	Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Asn	Ala	Ser	Ala	Ile	Glu	Xaa	Xaa	Leu
	50					55					60				
Xaa	Xaa	Leu	Xaa	Pro	Cys	Leu	Pro	Xaa	Xaa	Thr	Ala	Xaa	Pro	Xaa	Arg
65					70					75					80
Xaa	Pro	Ile	Xaa	Xaa	Xaa	Xaa	Gly	Asp	Trp	Xaa	Glu	Phe	Xaa	Xaa	Lys
			85						90					95	
Leu	Xaa	Phe	Tyr	Leu	Xaa	Xaa	Leu	Glu	Xaa	Xaa	Xaa	Xaa	Gln	Gln	
			100					105					110		

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AACAACTCA ATGCTGAAGA CGTTGAT

27

## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCAACGTCT TCAGCATT

18

## (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AACAACTCA ATTCTGAAGA CATGGAT

27

## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATCCATGTCT TCAGAATT

18

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CATGGGAACC ATATGTCAGG AT

22

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATCCTGACAT ATGGTTCC

18

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TGAACCATAT GTCAGG

16

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AATTCCTGAC ATATGGTTCA TGCA

24

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AATTCGAACC ATATGTCAGA

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AGCTTCTGAC ATATGGTTTCG

20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATCGAACCAT ATGTCAGATG CA

22

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TCTGACATAT GGTTCGAT

18

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATCCTGATGG AACGAAACCT TCGACTTCCA AACCTG

36

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAGTCGAAGG TTTCGTTCCA TCAGGAT

27

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATCCTGATGG AACGAAACCT TCGAACTCCA AACCTG

36

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:  
AGTTCGAAGG TTTCGTTCCA TCAGGAT 27

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:  
CTCGCATTCG TAAGGGCTGT CAAG 24

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:  
CCTTACGAAT GCGAGCAGGT TTGG 24

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:  
GAGAGCTTCG TAAGGGCTGT CAAG 24

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCTTACGAAG CTCTCCAGGT TTGG

24

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CACTTAGAAA ATGCA

15

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTTCTAAGT GCTTGACAGC

20

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AACTTAGAAA ATGCA

15

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TTTTCTAAGT TCTTGACAGC

20

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGTGATTGGA TGTCGAGAGG GTGCGGCCGT GGCAGAGGGC AGACATGG

48

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA CCATCAAG

48

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GATGATTGGA TGTCGAGAGG GTGCGGCCGT GGCAGAGGGC AGACATGG

48

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCAAG

48

## (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TACGAGATTA CGAAGAAT

18

## (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CGTAATCTCG TACCATGT

18

## (2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TTGGAGATTA CGAAGAAT

18

## (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CGTAATCTCC AACCATGT

18

## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TGCCTCAATA CCTGATGCA

19

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TCAGGTATTG AGGCAATTCT T

21

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AATTCTTGCC AGTCACCTGC CTTGAT

26

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCAGGTGACT GGCAAG

16

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AATTCCGGGA AAAACTGACG TTCTATCTGG TT

32

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CTCAAGGGAA ACCAGATAGA ACGTCAGTTT TTCCCGG

37

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCTTGAGC ACGCGCAGGA ACAACAGTAA TA

32

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AGCTTATTAC TGTTGTTTCCT GCGCGTG

27

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACCCTTGAGC AAGCGCAGGA ACAACAGTAA TA

32

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

AGCTTATTAC TGTTGTTTCCT GCGCTTG

27

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1				5				10						15	
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
			20				25						30		
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
		35					40					45			
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu
	50					55					60				
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg
65				70					75						80
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys
			85						90					95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 111 amino acids  
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	1	5	10	15
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp	Val	Asp	20	25	30	
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn	35	40	45	
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	50	55	60	
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	65	70	75	80
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys	85	90	95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	100	105	110		

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	1	5	10	15
Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp	Met	Asp	20	25	30	
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn	35	40	45	
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	50	55	60	
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	65	70	75	80
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys	85	90	95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	100	105	110		

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 111 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Val	Pro	1	5	10	15
Pro	Ala	Pro	Leu	Leu	Asp	Ser	Asn	Asn	Leu	Asn	Ser	Glu	Asp	Met	Asp	20	25	30	
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn	35	40	45	
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	50	55	60	
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	65	70	75	80
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys	85	90	95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	100	105	110		

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro	1	5	10	15
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp	20	25	30	
Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Leu	Ala	Phe	Val	35	40	45	
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	50	55	60	
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	65	70	75	80
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys	85	90	95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	100	105	110		

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro	1	5	10	15
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp	20	25	30	
Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	35	40	45	
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	50	55	60	
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	65	70	75	
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys	85	90	95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	100	105	110		

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro	1	5	10	15
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp	20	25	30	
Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala	Phe	Val	35	40	45	
Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	50	55	60	
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	65	70	75	
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys	85	90	95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	100	105	110		

## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1				5				10						15	
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
			20				25						30		
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
		35				40						45			
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
	50					55					60				
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65					70					75					80
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Arg	Lys
			85					90						95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	
			100					105					110		

## (2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1				5				10						15	
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
			20				25						30		
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
		35				40						45			
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
	50					55					60				
Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65					70					75					80
His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Arg	Lys
				85				90						95	

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln  
 100 105 110

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro  
 1 5 10 15  
 Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp  
 20 25 30  
 Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn  
 35 40 45  
 Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu  
 50 55 60  
 Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg  
 65 70 75 80  
 His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Glu Lys  
 85 90 95  
 Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
 100 105 110

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro  
 1 5 10 15  
 Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp  
 20 25 30  
 Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn  
 35 40 45  
 Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu  
 50 55 60  
 Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg  
 65 70 75 80  
 His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Glu Lys

	85		90		95									
Leu	Thr	Phe	Tyr	Leu	Val	Ser	Leu	Glu	His	Ala	Gln	Glu	Gln	Gln
			100					105					110	

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1				5				10						15	
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
			20					25					30		
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
		35					40					45			
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
	50					55					60				
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65					70				75						80
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys
				85					90					95	
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
				100				105					110		

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1				5				10						15	
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
			20					25					30		
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
		35					40					45			
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
	50					55					60				
Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65					70				75						80

His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys  
85 90 95

Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
100 105 110

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro  
1 5 10 15  
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp  
20 25 30  
Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn  
35 40 45  
Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala Ile Leu  
50 55 60  
Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg  
65 70 75 80  
His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys  
85 90 95  
Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln Gln  
100 105 110

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro  
1 5 10 15  
Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp Val Asp  
20 25 30  
Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val  
35 40 45  
Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu  
50 55 60

Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg  
 65 70 75 80  
 His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys  
 85 90 95  
 Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln  
 100 105 110

## (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro  
 1 5 10 15  
 Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp  
 20 25 30  
 Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val  
 35 40 45  
 Arg Ala Val Lys His Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu  
 50 55 60  
 Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg  
 65 70 75 80  
 His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys  
 85 90 95  
 Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln  
 100 105 110

## (2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Val Pro  
 1 5 10 15  
 Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp Met Asp  
 20 25 30  
 Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala Phe Val  
 35 40 45  
 Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu

50		55		60											
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg
65					70					75					80
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys
				85					90					95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	
			100					105					110		

## (2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met	Ala	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys
1				5					10					15	
Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp
			20					25					30		
Gln	Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala
		35					40					45			
Phe	Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65				70					75					80	
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

## (2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Met	Ala	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys
1				5					10					15	
Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp
			20					25					30		



Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala  
           35                          40                          45  
 Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala  
           50                          55                          60  
 Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65                          70                          75                          80  
 Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
                           85                          90                          95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
                           100                          105                          110  
 Gln

## (2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys  
 1                          5                          10                          15  
 Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp  
           20                          25                          30  
 Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala  
           35                          40                          45  
 Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala  
           50                          55                          60  
 Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65                          70                          75                          80  
 Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
                           85                          90                          95  
 Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln  
                           100                          105                          110  
 Gln

## (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Ala	Ile	Glu	Ser
	50					55					60				
Ile	Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Thr	Arg	His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg
				85					90					95	
Arg	Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln
			100					105					110		

Gln

## (2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Ala	Ile	Glu	Ser
	50					55					60				
Ile	Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Thr	Arg	His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg
				85					90					95	
Arg	Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln
			100					105					110		

Gln

## (2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5				10						15	
Val	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Ser	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20				25						30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Ala	Ile	Glu	Ser
	50					55					60				
Ile	Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Thr	Arg	His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg
				85					90					95	
Arg	Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5				10						15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20				25						30		
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
 20 25 30  
 Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
 35 40 45  
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp  
 20 25 30  
 Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala  
 35 40 45  
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala

50		55		60											
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65				70				75							80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
			85					90						95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1			5					10						15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20				25						30		
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35				40					45				
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50				55					60					
Ile	Leu	Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65				70					75						80
Ser	Arg	His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
			85					90						95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1			5					10						15	

Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp  
                     20                    25                    30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala  
                     35                    40                    45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
                     50                    55                    60

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
                     65                    70                    75                    80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
                     85                    90                    95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
                     100                    105                    110

Gln

## (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
   1                    5                    10                    15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
                     20                    25                    30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
                     35                    40                    45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
                     50                    55                    60

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
                     65                    70                    75                    80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
                     85                    90                    95

Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln  
                     100                    105                    110

Gln

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Val	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Ser	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Ser	Leu	Glu	His	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

## (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1           5           10           15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
          20           25           30
Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
          35           40           45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
          50           55           60
Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65           70           75           80
Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
          85           90           95
Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln
          100          105          110
Gln

```

## (2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA      60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC      120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA      180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC      240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG      300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG                               339

```

## (2) INFORMATION FOR SEQ ID NO:98:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTTCCCTTGA GCACGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
---	----

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTTCCCTTGA GCACGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 339 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGGT TCCACCTGCA	60
CCTTTGCTGG ACAGTAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGGT TCCACCTGCA	60
CCTTTGCTGG ACAGTAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGGT TCCACCTGCA	60
CCTTTGCTGG ACAGTAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120

CTTCGACTTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTTCCCTTGA GCACGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA AGAGACCACC TGCACCTTTG	60
CTGGACCCGA ACAACCTCAA TGCTGAAGAC GTCGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGCAATT	180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA	240
CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT	300
CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG	333

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA AGAGACCACC TAACCCTTTG	60
CTGGACCCGA ACAACCTCAA TTCTGAAGAC ATGGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGCAATT	180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA	240
CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT	300
CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG	333

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA AGGTTCCACC TGCACCTTTG	60
CTGGACAGTA ACAACCTCAA TTCCGAAGAC ATGGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGCAATT	180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA	240
CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT	300
CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG	333

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAACG AAACCTTCGA	120
CTTCCAAACC TGCTCGCATT CGTAAGGGCT GTCAAGAACT TAGAAAATGC ATCAGCAATT	180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA	240
CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT	300
CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG	333

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAACG AAACCTTCGA	120
CTTCCAAACC TGGAGAGCTT CGTAAGGGCT GTCAAGAACT TAGAAAATGC ATCAGCAATT	180

GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA 240  
 CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT 300  
 CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG 333

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG 60  
 CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAACG AAACCTTCGA 120  
 ACTCCAAACC TGCTCGCATT CGTAAGGGCT GTCAAGCACT TAGAAAATGC ATCAGCAATT 180  
 GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA 240  
 CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT 300  
 CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG 333

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG 60  
 CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAAAA TAACCTTCGT 120  
 CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGGTATT 180  
 GAGGCAATTC TTCGTAATCT CCAACCATGT CTGCCCTCTG CCACGGCCGC ACCCTCTCGA 240  
 CATCCAATCA TCATCAAGGC AGGTGACTGG CAAGAATTCC GTCGTAAACT GACCTTCTAT 300  
 CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG 333

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGGTATT	180
GAGGCAATTC TTCGTAATCT CGTACCATGT CTGCCCTCTG CCACGGCCGC ACCCTCTCGA	240
CATCCAATCA CCATCAAGGC AGGTGACTGG CAAGAATTCC GTCGTAAACT GACCTTCTAT	300
CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG	333

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGCAATT	180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA	240
CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GGGAAAAACT GACGTTCTAT	300
CTGGTTACCC TTGAGCAAGC GCAGGAACAA CAG	333

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGCAATT	180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA	240

CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GGGAAAACT GACGTTCTAT 300  
 CTGGTTTCCC TTGAGCACGC GCAGGAACAA CAG 333

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA AGAGACCACC TGCACCTTTG 60  
 CTGGACCCGA ACAACCTCAA TGCTGAAGAC GTCGATATCC TGATGGAACG AAACCTTCGA 120  
 CTTCCAAACC TGGAGAGCTT CGTAAGGGCT GTCAAGAACT TAGAAAATGC ATCAGCAATT 180  
 GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA 240  
 CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT 300  
 CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG 333

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA AGAGACCACC TAACCCTTTG 60  
 CTGGACCCGA ACAACCTCAA TTCTGAAGAC ATGGATATCC TGATGGAACG AAACCTTCGA 120  
 ACTCCAAACC TGCTCGCATT CGTAAGGGCT GTCAAGCACT TAGAAAATGC ATCAGCAATT 180  
 GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA 240  
 CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT 300  
 CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG 333

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA AGGTTCCACC TGCACCTTTG	60
CTGGACAGTA ACAACCTCAA TTCCGAAGAC ATGGATATCC TGATGGAACG AAACCTTCGA	120
CTTCCAAACC TGCTCGCATT CGTAAGGGCT GTCAAGAACT TAGAAAATGC ATCAGCAATT	180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA	240
CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT	300
CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG	333

## (2) INFORMATION FOR SEQ ID NO:119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGGTATT	180
GAGGCAATTC TTCGTAATCT CCAACCATGT CTGCCCTCTG CCACGGCCGC ACCCTCTCGA	240
CATCCAATCA TCATCAAGGC AGGTGACTGG CAAGAATTCC GGGAAAAACT GACGTTCTAT	300
CTGGTTACCC TTGAGCAAGC GCAGGAACAA CAG	333

## (2) INFORMATION FOR SEQ ID NO:120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGGTATT	180
GAGGCAATTC TTCGTAATCT CGTACCATGT CTGCCCTCTG CCACGGCCGC ACCCTCTCGA	240
CATCCAATCA CCATCAAGGC AGGTGACTGG CAAGAATTCC GGGAAAAACT GACGTTCTAT	300

CTGGTTACCC TTGAGCAAGC GCAGGAACAA CAG

333

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGGTATT	180
GAGGCAATTC TTCGTAATCT CGTACCATGT CTGCCCTCTG CCACGGCCGC ACCCTCTCGA	240
CATCCAATCA CCATCAAGGC AGGTGACTGG CAAGAATTCC GGGAAAAACT GACGTTCTAT	300
CTGGTTTCCC TTGAGCACGC GCAGGAACAA CAG	333

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC	240
ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC	300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAG	339

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC	240
ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC	300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAG	339

## (2) INFORMATION FOR SEQ ID NO:124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGGT TCCACCTGCA	60
CCTTTGCTGG ACAGTAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGCT CGCATTCTGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC	240
ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC	300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAG	339

## (2) INFORMATION FOR SEQ ID NO:125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG	60
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTGAT GGAAAATAAC	120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG	60
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTGAT GGAAAATAAC	120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG	60
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTGAT GGAAAATAAC	120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTTCCCTTGA GCACGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn

1		5		10		15									
Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro	Pro
			20					25					30		
Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp	Ile
		35					40					45			
Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn	Arg
	50					55					60				
Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	Lys
65					70					75					80
Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	His
				85					90					95	
Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys	Leu
			100					105					110		
Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	Thr	Thr
		115					120					125			
Leu	Ser	Leu	Ala	Ile	Phe										

## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn or Ile"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met, Ala, or Ile"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /note= "Xaa at position 20 is Ile, Pro, or Leu"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile, Ala, or Leu"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 25
  - (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr  
or His"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 29
  - (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln,  
Arg, Val, or Leu"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 32
  - (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu,  
Ala, Asn, or Arg"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 34
  - (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu  
or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 37
  - (D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe,  
Pro, or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 38
  - (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn  
or Ala"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 42
  - (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,  
Ala, Ser, Asp, or Asn"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 45
  - (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,  
Val, or Met"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 46
  - (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp  
or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 49
  - (D) OTHER INFORMATION: /note= "Xaa at position 49 is Met,  
Ile, Leu, or Asp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 50
  - (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu  
or Asp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 51

(D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn,  
Arg, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 55

(D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg,  
Leu, or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 56

(D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro  
or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 59

(D) OTHER INFORMATION: /note= "Xaa at position 59 is Glu  
or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 60

(D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala  
or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 62

(D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn  
Val, or Pro"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 63

(D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg  
or His"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 65

(D) OTHER INFORMATION: /note= "Xaa at position 65 is Val  
or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 67

(D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser,  
Asn, His, or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 69

(D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln  
or Glu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 73

(D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala  
or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 76

- (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser, Ala, or Pro"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 79  
(D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys, Arg, or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 82  
(D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu, Glu, Val, or Trp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 85  
(D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu or Val"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 87  
(D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu, Ser, or Trp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 88  
(D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala or Trp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 91  
(D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala or Pro"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 93  
(D) OTHER INFORMATION: /note= "Xaa at position 93 is Pro or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 95  
(D) OTHER INFORMATION: /note= "Xaa at position 95 is His or Thr"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 98  
(D) OTHER INFORMATION: /note= "Xaa at position 98 is His, Ile, or Thr"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 100  
(D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 101  
(D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp,



Ala, or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 105  
(D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn  
or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 109  
(D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg,  
Glu, or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 112  
(D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr  
or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 116  
(D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys,  
Val, Trp, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 117  
(D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr  
or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 120  
(D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn,  
Gln, or His"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 123  
(D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala  
or Glu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys
1				5					10					15	
Ser	Xaa	Xaa	Xaa	Asp	Glu	Xaa	Ile	Xaa	His	Leu	Lys	Xaa	Pro	Pro	Xaa
			20					25					30		
Pro	Xaa	Leu	Asp	Xaa	Xaa	Asn	Leu	Asn	Xaa	Glu	Asp	Xaa	Xaa	Ile	Leu
		35					40					45			
Xaa	Xaa	Xaa	Asn	Leu	Arg	Xaa	Xaa	Asn	Leu	Xaa	Xaa	Phe	Xaa	Xaa	Ala
		50				55						60			
Xaa	Lys	Xaa	Leu	Xaa	Asn	Ala	Ser	Xaa	Ile	Glu	Xaa	Ile	Leu	Xaa	Asn
65					70					75				80	
Leu	Xaa	Pro	Cys	Xaa	Pro	Xaa	Xaa	Thr	Ala	Xaa	Pro	Xaa	Arg	Xaa	Pro
			85						90					95	
Ile	Xaa	Ile	Xaa	Xaa	Gly	Asp	Trp	Xaa	Glu	Phe	Arg	Xaa	Lys	Leu	Xaa
			100					105						110	

Phe Tyr Leu Xaa Xaa Leu Glu Xaa Ala Gln Xaa Gln Gln Thr Thr Leu  
 115 120 125

Ser Leu Ala Ile Phe  
 130

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- or Met-Ala may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met, Ala, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "Xaa at position 6 is Ile, Pro, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile, Ala, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln, Arg, Val, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu, Ala, Asn, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 20
  - (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 23
  - (D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe, Pro, or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 24
  - (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn or Ala"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 28
  - (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly, Ala, Ser, Asp, or Asn"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 31
  - (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln, Val, or Met"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 32
  - (D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 35
  - (D) OTHER INFORMATION: /note= "Xaa at position 35 is Met, Ile, Leu, or Asp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 36
  - (D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu or Asp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 37
  - (D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn, Arg, or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 41
  - (D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg, Leu, or Thr"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 42
  - (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
  - (B) LOCATION: 45

- (D) OTHER INFORMATION: /note= "Xaa at position 45 is Glu  
or Leu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 46  
(D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala  
or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 48  
(D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn,  
Val, or Pro"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 49  
(D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg  
or His"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 51  
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Val  
or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 53  
(D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser,  
Asn, His, or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 55  
(D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln  
or Glu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 59  
(D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala  
or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 62  
(D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,  
Ala, or Pro"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 65  
(D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,  
Arg, or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 67  
(D) OTHER INFORMATION: /note= "Xaa at position 67 is Leu,  
Glu, or Val"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 68  
(D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,

Glu, Val, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 71
- (D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 73
- (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu, Ser, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 74
- (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 77
- (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 79
- (D) OTHER INFORMATION: /note= "Xaa at position 79 is Pro or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 81
- (D) OTHER INFORMATION: /note= "Xaa at position 81 is His or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 84
- (D) OTHER INFORMATION: /note= "Xaa at position 84 is His, Ile, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 86
- (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 87
- (D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp, Ala, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 91
- (D) OTHER INFORMATION: /note= "Xaa at position 91 is Asn or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 95
- (D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg, Glu, or Leu"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 98
- (D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr or Gln"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 102
- (D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys, Val, Trp, or Ser"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 103
- (D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr or Ser"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 106
- (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn, Gln, or His"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 109
- (D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala or Glu"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asn	Cys	Ser	Xaa	Xaa	Xaa	Asp	Glu	Xaa	Ile	Xaa	His	Leu	Lys	Xaa	Pro	1	5	10	15
Pro	Xaa	Pro	Xaa	Leu	Asp	Xaa	Xaa	Asn	Leu	Asn	Xaa	Glu	Asp	Xaa	Xaa	20	25	30	
Ile	Leu	Xaa	Xaa	Xaa	Asn	Leu	Arg	Xaa	Xaa	Asn	Leu	Xaa	Xaa	Phe	Xaa	35	40	45	
Xaa	Ala	Xaa	Lys	Xaa	Leu	Xaa	Asn	Ala	Ser	Xaa	Ile	Glu	Xaa	Ile	Leu	50	55	60	
Xaa	Asn	Xaa	Xaa	Pro	Cys	Xaa	Pro	Xaa	Xaa	Thr	Ala	Xaa	Pro	Xaa	Arg	65	70	75	80
Xaa	Pro	Ile	Xaa	Ile	Xaa	Xaa	Gly	Asp	Trp	Xaa	Glu	Phe	Arg	Xaa	Lys	85	90	95	
Leu	Xaa	Phe	Tyr	Leu	Xaa	Xaa	Leu	Glu	Xaa	Ala	Gln	Xaa	Gln	Gln	100	105	110		

## (2) INFORMATION FOR SEQ ID NO:131:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTAGCCACGG CCGCACCCAC GCGACATCCA ATCCATATCA AGGACGGTGA CTGGAATG 58

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

TTAACATTCC AGTCACCGTC CTTGATATGG ATTGGATGTC GCGTGGGTGC GGCCGTGG 58

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAGGAGATAT ATCCATGAAC TGCTCTAAC 29

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Asn Cys Ser Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln

1	5	10	15												
Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln
		20						25					30		
Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe
		35					40					45			
Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile
	50					55					60				
Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr
65					70					75				80	
Arg	His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg
				85					90					95	
Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln
			100					105					110		
Thr	Thr	Leu	Arg	Leu	Ala	Ile	Phe								
		115					120								

## (2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 71 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

AATTCGTCG TAAACTGACC TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGA	60
CCACTCTGTC G	71

## (2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 71 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CTAGCGACAG AGTGGTCTGT TGAGCCTGCG CGTTCTCCAA GGTTCAGG TAGAAGGTCA	60
GTTTACGACG G	71

## (2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln
1				5					10					15	
Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln
			20					25					30		
Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe
		35					40					45			
Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile
	50					55				60					
Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr
65					70					75					80
Arg	His	Pro	Ile	His	Ile	Lys	Ala	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg
				85					90					95	
Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Met	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln
1				5					10					15	
Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln
			20					25					30		
Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe
		35					40					45			
Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile
	50					55				60					
Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala					
65					70					75					

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CTAGCCACGG CCGCACCCAC GCGACATCCA ATCCATATCA AGGCTGGTGA CTGGAATG 58

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AATTCATTCC AGTCACCAGC CTTGATATGG ATTGGATGTC GCGTGGGTGC GGCCGTGG 58

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

AATTCCGTCG TAAACTGACC TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT 60

AATA 64

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AGCTTATTAC TGTTGAGCCT GCGCGTTCTC CAAGGTTTTC AGATAGAAGG TCAGTTTACG 60

ACGG 64

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ATGGCTCCAA TGACTCAGAC TACTTCTCTT AAGACTTCTT GGGTTAACTG CTCTAACATG	60
ATCGATGAAA TTATAACACA CTTAAAGCAG CCACCTTTGC CTTTGCTGGA CTTCAACAAC	120
CTCAATGGGG AAGACCAAGA CATTCTGATG GAAAATAACC TTCGAAGGCC AAACCTGGAG	180
GCATTCAACA GGGCTGTCAA GAGTTTACAG AATGCATCAG CAATTGAGAG CATTCTTAAA	240
AATCTCCTGC CATGTCTGCC CCTGGCCACG GCCGCACCCA CGCGACATCC AATCCATATC	300
AAGGACGGTG ACTGGAATGA ATTCCGTCGT AAAGTGACCT TCTATCTGAA AACCTTGGAG	360
AACGCGCAGG CTCAACAGAC CACTCTGTCTG CTAGCGATCT TTTAATAA	408

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ATC GAT GAA ATC ATC ACC CAC CTG AAG CAG CCA CCG CTG CCG CTG CTG	48
Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro Leu Pro Leu Leu	
1 5 10 15	
GAC TTC AAC AAC CTC AAT GGT GAA GAC CAA GAT ATC CTG ATG GAA AAT	96
Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile Leu Met Glu Asn	
20 25 30	
AAC CTT CGT CGT CCA AAC CTC GAG GCA TTC AAC CGT GCT GTC AAG TCT	144
Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg Ala Val Lys Ser	
35 40 45	
CTG CAG AAT GCA T	157
Leu Gln Asn Ala	
50	

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro Leu Pro Leu Leu  
 1 5 10 15  
 Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile Leu Met Glu Asn  
 20 25 30  
 Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg Ala Val Lys Ser  
 35 40 45  
 Leu Gln Asn Ala  
 50

## (2) INFORMATION FOR SEQ ID NO:147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CCATGGCTCC AATGACTCAG ACTACTTCTC TTAAGACTTC TTGGGTAAAC TGCTCTAACA 60  
 TGATCGATGA AATTATAACA CACTTAAAGC AGCCACCTTT GCCTTTGCTG GACTTCAACA 120  
 ACCTCAATGG GGAAGACCAA GACATTCTGA TGGAAAATAA CCTTCGAAGG CCAAACCTGG 180  
 AGGCATTCAA CAGGGCTGTC AAGAGTTTAC AGAATGCATC AGCAATTGAG AGCATTCTTA 240  
 AAAATCTCCT GCCATGTCTG CCCCTGGCCA CGGCCGCACC CACGCGACAT CCAATCCATA 300  
 TCAAGGACGG TGA CTGGAAT GAATTCCGTC GTAAACTGAC CTTCTATCTG AAAACCTTGG 360  
 AGAACGCGCA GGCTCAACAG ACCACTCTGT CGCTAGCGAT CTTTAAATAA GCTT 414

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

AAGCTTATTA AAAGATCGCT AGCGACAGAG TGGTCTGTTG AGCCTGCGCG TTCTCCAAGG 60  
 TTTTCAGATA GAAGGTCAGT TTACGACGGA ATTCATTCCA GTCACCGTCC TTGATATGGA 120  
 TTGGATGTCG CGTGGGTGCG GCCGTGGCCA GGGGCAGACA TGGCAGGAGA TTTTAAAGAA 180  
 TGCTCTCAAT TGCTGATGCA TTCTGTAAAC TCTTGACAGC CCTGTTGAAT GCCTCCAGGT 240  
 TTGGCCTTCG AAGGTTATTT TCCATCAGAA TGTCTTGGTC TTCCCATTTG AGGTTGTTGA 300  
 AGTCCAGCAA AGGCAAAGGT GGCTGCTTTA AGTGTGTTAT AATTTTCATCG ATCATGTTAG 360

AGCAGTTAAC CCAAGAAGTC TTAAGAGAAG TAGTCTGAGT CATTGGAGCC ATGG

414

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 81 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ATGATGATTA CTCTGCGCAA ACTTCCTCTG GCGGTTGCCG TCGCAGCGGG CGTAATGTCT 60

GCTCAGGCCA TGGCTAACTG C 81

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 81 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GCAGTTAGCC ATGGCCTGAG CAGACATTAC GCCCGCTGCG ACGGCAACCG CCAGAGGAAG 60

TTTGCGCAGA GTAATCATCA T 81

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CATGGCTAAC TGCTCTAACA TGAT 24

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

CGATCATGTT AGAGCAGTTA GC

22

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ATGGCTAACT GC

12

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met Ala Asn Cys  
1

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GCCGATACCG CGGCATACTC CCACCATTTCA GAGA

34

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GCCGATAAGA TCTAAAACGG GTATGGAGAA ACA

33

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ATAGTCTTCC CCAGATATCT AACGCTTGAG

30

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CAATACCTGA TGC GTTTTCT AAGT

24

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GGTTTCGTTC CATCAGAATG TCCATGTCTT CAG

33

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC

60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC 120  
 CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAACGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 338 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ACATTTGATG GAACGAAACC 120  
 TTCGAACTCC AAACCTGCTC GCATTCGTAA GGGCTGTCAA GCACTTAGAA AACGCATCAG 180  
 GTATTGAGGC AATTCTTCGT AATCTCCAAC CATGTCTGCC CTCTGCCACG GCCGCACCCT 240  
 CTCGACATCC AATCATCATC AAGGCAGGTG ACTGGCAAGA ATTCCGGGAA AAACTGACGT 300  
 TCTATCTGGT TACCCTTGAG CAAGCGCAGG AACAACAG 338

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

CATGGCTAAC TGCTCTAACA TGATCGATGA AATTATAACA 40

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 45 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:



CTTTAAGTGT GTTATAATTT CATCGATCAT GTTAGAGCAG TTAGC

45

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CACTTAAAGC AGCCACCTTT GCCTTTGCTG GACTTC

36

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GAGGTTGTTG AAGTCCAGCA AAGGCAAAGG TGGCTG

36

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

AACAACCTCA ATGACGAAGA CATGTCT

27

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

AGACATGTCT TCGTCATT

18

## (2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

TGAACCATAT GTCAGG

16

## (2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

AATTCCTGAC ATATGGTTCA TGCA

24

## (2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

CATGGCAAAC TGCTCTATAG CTATCGATGA AATTATACAT

40

## (2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

CTTTAAGTGA TGTATAATTT CATCGATAGC TATAGAGCAG TTTGC

45

## (2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CATGGCAAAC TGCTCTATAA TCATCGATGA AATTATACAT

40

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

CTTTAAGTGA TGTATAATTT CATCGATGAT TATAGAGCAG TTTGC

45

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

ATCCTGGACG AACGAAACCT TCGAACTCCA AACCTG

36

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AGTTCGAAGG TTTCGTTCGT CCAGGAT

27

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

ATCCTGATCG AACGAAACCT TCGAACTCCA AACCTG

36

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

AGTTCGAAGG TTTCGTTCCA TCAGGAT

27

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ATCCTGCTGG AACGAAACCT TCGAACTCCA AACCTG

36

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

AGTTCGAAGG TTTCGTTCCA GCAGGAT

27

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

AACAACCTCA ATTCTGAAGA CGTTGAT

27

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

ATCAACGTCT TCAGAATT

18

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CGCGCCATGG CTAACFGCTC TATAATGATC GATGAAGCAA TACATCACTT A

51

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CGCGTCGATA AGCTTATT

18

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GGAGATATAT CCATGGCT

18

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

TCGGTCCATC AGAATAGACA TGTCTTCAGC ATTGAGGTTG TT

42

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

TCGGTCCATC AGAATAGAAA CGTCTTCAGC ATTGAGGTTG TT

42

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

TCGGTCCATC AGAATAGACA TGTCTTCGTC ATTGAGGTTG TT

42

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

TCGGTCCATC AGAATAGAAA CGTCTTCGTC ATTGAGGTTG TT

42

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TCGGTCCATC AGAATAGACA TGTCTTCAGA ATTGAGGTTG TT

42

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TCGGTCCATC AGAATAGAAA CGTCTTCAGA ATTGAGGTTG TT

42

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCCGT

48

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

AATTCTTGCC AGTCACCTGC ACGGAT

26

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATGGGTGACT GGCAAG

16

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

AATTCTTGCC AGTCACCCAT ACGGAT

26

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CATGGCTAAC TGCTCTATTA TGATCGATGA AGCAATACAT

40

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:



CTTTAAGTGA TGTATTGCTT CATCGATCAT AATAGAGCAG TTAGC

45

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

CACTTAAAGG TACCACCTCG CCCTTCCCTG GACCCG

36

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GAGGTTGTTC GGGTCCAGGG AAGGGCGAGG TGGTAC

36

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

CACTTAAAGA GACCACCTGC ACCTTCCCTG GACCCG

36

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GAGGTTGTTC GGGTCCAGGG AAGGTGCAGG TGGTCT

36

## (2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

AACAACCTCA ATGACGAAGA CATGGAT

27

## (2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

ATCCATGTCT TCGTCATT

18

## (2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

AACAACCTCA .ATGACGAAGA CGTCGAT

27

## (2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

ATCGACGTCT TCGTCATT

18

## (2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

AACAACCTCA ATGACGAAGA CATGTCT

27

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

AGACATGTCT TCGTCATT

18

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

AACAACCTCA ATGACGAAGA CGTCTCT

27

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGAGACGTCT TCGTCATT

18

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

ATCCTGATGG ACCGAAACCT TCGACTTCCA AACCTG

36

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

AAGTCGAAGG TTTCGGTCCA TCAGGAT

27

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ATCCTGATGG ACCGAAACCT TCGACTTAGC AACCTG

36

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CCTTACGAAG CTCTCCAGGT TGCT

24

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

CGTAATCTCT GGCCATGT

18

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

CCAGAGATTA CGAAGAAT

18

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

AATTCGGGA AAAACTGCAA TTCTATCTGT GG

32

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTCAAGGGTC CACAGATAGA ATTGCAGTTT TTCCCGG

37

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

AATTCGGGA AAAACTGCAA TTCTATCTGG TT

32

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 37 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

CTCAAGGGTA ACCAGATAGA ATTGCAGTTT TTCCCGG

37

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

AATTCGGGA AAAACTGACG TTC

23

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 28 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

AACCAGATAG AACGTCAGTT TTTCCCGG

28

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:  
TATCTGGTTA CCCTTGAGTA ATA 23

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:  
AGCTTATTAC TTCAAGGGT 19

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:  
AATTCGGGA AAAACTGCAA TTC 23

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:  
AACCAGATAG AATTGCAGTT TTTCCCGG 28

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

CGATCATTAT AGAGCAGTTA GCCTTGTCAT CGTCGTCCTT GTAATCAGTT TCTGGATATG 60  
C 61

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

CATGGCATAT CCAGAACTG ATTACAAGGA CGACGATGAC AAGGCTAACT GCTCTATAAT 60  
GAT 63

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

AATTCCGGCT TAAACTGCAA TTCTATCTGT CT 32

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

CTCAAGGGTA GACAGATAGA ATTGCAGTTT AAGCCGG 37

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

TCTCTTGAGC AAGCGCAGGA ACAACAGTAA TA

32

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

CATGGCAAAC TGCTCTATAA TACTCGATGA AGCAATACAT

40

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CTTTAAGTGA TGTATTGCTT CATCGAGTAT TATAGAGCAG TTTGC

45

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

CATGGCAAAC TGCTCTATAA TGCCAGATGA AGCAATACAT

40

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

CTTTAAGTGA TGTATTGCTT CATCTGGCAT TATAGAGCAG TTTGC

45

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 41 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

CATGGCAAAC TGCTCTATAA TGATCGATGA AACTGATACA T

41

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 45 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CTTTAAGTGA TGTATCAGTT CATCGATCAT TATAGAGCAG TTTGC

45

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

CACTTAAAGA TACCACCTAA CCCTAGCCTG GACAGT

36

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GAGGTTAGCA CTGTCCAGGC TAGGGTTAGG TGGTAT

36

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GCTAACCTCA ATTCCGAAGA CGTCTCT

27

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

AGAGACGTCT TCGGAATT

18

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

ATCCTGATGG ACTCCAACCT TCGAACTCCA AACCTG

36

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

AGTTCGAAGG TTGGAGTCCA TCAGGAT

27

## (2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GTTCCCTATT GGACGGCCCC TCCCTCTCGA ACACCAATCA CGATCAAG

48

## (2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

CGTGATTGGT GTTCGAGAGG GAGGGGCCGT CCAATAGGGA ACACATGG

48

## (2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

CTCGCATTC CACATGCTTC TAAG

24

## (2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

CTCGCATTC CACATGCTGT CAAG

24

## (2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

ATGTGGGAAT GCGAGCAGGT TTGG

24

(2) INFORMATION FOR SEQ ID NO:247:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

TTTTCTAATT GCTTAGAAGC

20

(2) INFORMATION FOR SEQ ID NO:248:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

CAATTAGAAA ATGCA

15

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TTTTCTAATT GCTTGACAGC

20

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

TCAGGTATTG AGCCAATTCT T

21

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TGGCTCAATA CCTGATGCA

19

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

TCTAATCTCC AACCATGT

18

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

TTGGAGATTA GAAAGAAT

18

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CTCAAGAGAA GACAGATAGA ATTGCAGTTT AAGCCGG

37

(2) INFORMATION FOR SEQ ID NO:255:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

CATGGCTAAC TGCTCTATAA TGATCGATGA AATTATACAT

40

(2) INFORMATION FOR SEQ ID NO:256:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

AATTCCGGCT TAAACTGCAA TTCTATCTGT CTACCCTTTA ATA

43

(2) INFORMATION FOR SEQ ID NO:257:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

AGCTTATTAA AGGGTAGACA GATAGAATTG CAGTTTAAGC CGG

43

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

AATTCGGGCT TAAACTGCAA TTCTATCTGT CTACCCTTTA ATA

43

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Met	Ala	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys
1				5					10					15	

Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Asp	Glu	Asp
			20					25					30		

Met	Ser	Ile	Leu	Met	Asp	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala
		35					40					45			

Phe	Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser
	50					55					60				

Ile	Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro
65					70					75					80

Thr	Arg	His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg
				85					90					95	

Arg	Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Met	Ala	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys
1				5					10					15	

Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Asp	Glu	Asp
			20					25					30		



Met Ser Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala  
                   35                  40                  45

Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser  
       50                              55                  60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro  
  65                              70                  75                  80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg  
                               85                  90                  95

Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln  
                   100                  105                  110

Gln

## (2) INFORMATION FOR SEQ ID NO:261:

- (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 113 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys  
  1                  5                  10                  15

Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Asp Glu Asp  
                   20                  25                  30

Met Ser Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala  
                   35                  40                  45

Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser  
       50                              55                  60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro  
  65                              70                  75                  80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg  
                               85                  90                  95

Arg Lys Leu Thr Phe Tyr Leu Trp Thr Leu Glu Asn Ala Gln Ala Gln  
                   100                  105                  110

Gln

## (2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 113 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys  
 1 5 10 15  
 Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Asp Glu Asp  
 20 25 30  
 Met Ser Ile Leu Met Asp Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala  
 35 40 45  
 Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser  
 50 55 60  
 Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro  
 65 70 75 80  
 Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg  
 85 90 95  
 Arg Lys Leu Thr Phe Tyr Leu Trp Thr Leu Glu Asn Ala Gln Ala Gln  
 100 105 110  
 Gln

## (2) INFORMATION FOR SEQ ID NO:263:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys  
 1 5 10 15  
 Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Asp Glu Asp  
 20 25 30  
 Met Ser Ile Leu Met Asp Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala  
 35 40 45  
 Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser  
 50 55 60  
 Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro  
 65 70 75 80  
 Thr Arg Arg Pro Ile Ile Ile Arg Asp Gly Asp Trp Asn Glu Phe Arg  
 85 90 95  
 Arg Lys Leu Thr Phe Tyr Leu Trp Thr Leu Glu Asn Ala Gln Ala Gln  
 100 105 110  
 Gln

## (2) INFORMATION FOR SEQ ID NO:264:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Met	Ala	Asn	Cys	Ser	Ile	Ala	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Met	Ala	Asn	Cys	Ser	Ile	Ile	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln

105

Gln

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
20 25 30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Met Ala Asn Cys Ser Ile Ala Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
20 25 30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln

## (2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Met Ala Asn Cys Ser Ile Ile Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
 20 25 30  
 Val Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
 35 40 45  
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln

## (2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
                     20                    25                    30

Met Asp Ile Leu Ile Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
                     35                    40                    45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
                     50                    55                    60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
   65                    70                    75                    80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
                     85                    90                    95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
                     100                    105                    110

Gln

## (2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
   1                    5                    10                    15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
                     20                    25                    30

Met Asp Ile Leu Leu Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
                     35                    40                    45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
                     50                    55                    60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
   65                    70                    75                    80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
                     85                    90                    95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
                     100                    105                    110

Gln

## (2) INFORMATION FOR SEQ ID NO:271:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Asp	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Met	Ala	Asn	Cys	Ser	Ile	Ala	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Ile	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Met	Ala	Asn	Cys	Ser	Ile	Ile	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Ile	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met	Ala	Asn	Cys	Ser	Ile	Ala	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Leu	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg



				85						90					95
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Met	Ala	Asn	Cys	Ser	Ile	Ile	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Leu	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Met	Ala	Asn	Cys	Ser	Ile	Ala	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Asp	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln

## (2) INFORMATION FOR SEQ ID NO:277:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Met Ala Asn Cys Ser Ile Ile Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
 20 25 30  
 Val Asp Ile Leu Asp Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
 35 40 45  
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln

## (2) INFORMATION FOR SEQ ID NO:278:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys
1				5					10					15	
Val	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Ser	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

## (2) INFORMATION FOR SEQ ID NO:279:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys
1				5					10					15	
Val	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Ser	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Gln	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

## (2) INFORMATION FOR SEQ ID NO:280:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
			20					25					30		
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asn	Glu	Asp
			20					25					30		
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

## (2) INFORMATION FOR SEQ ID NO:282:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20					25					30		
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

## (2) INFORMATION FOR SEQ ID NO:283:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
			20					25					30		
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro

65		70		75		80									
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
			85						90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:284:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20					25					30		
Met	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50				55					60					
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65				70					75					80	
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
			20					25					30		

Met Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
 35 40 45  
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln

## (2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
 20 25 30  
 Met Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
 35 40 45  
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln

## (2) INFORMATION FOR SEQ ID NO:287:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	1	5	10	15
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp	20	25	30	
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	85	90	95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	100	105							

## (2) INFORMATION FOR SEQ ID NO:288:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Met	Asp	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys	1	5	10	15
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp	20	25	30	
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	85	90	95	
Glu	Lys	Leu	Gln	Phe	Tyr	Leu	Val	Thr	Leu	Glu	100	105							

## (2) INFORMATION FOR SEQ ID NO:289:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
			20					25					30		
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Gln	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

## (2) INFORMATION FOR SEQ ID NO:290:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Met	Asp	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu					
			100					105							

## (2) INFORMATION FOR SEQ ID NO:291:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

[illegible]

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Met 1	Ala	Asn	Cys	Ser 5	Ile	Met	Ile	Asp	Glu 10	Ile	Ile	His	His	Leu 15	Lys
Val	Pro	Pro	Arg 20	Pro	Ser	Leu	Asp	Pro 25	Asn	Asn	Leu	Asn	Ala 30	Glu	Asp
Val	Asp	Ile 35	Leu	Met	Glu	Arg	Asn 40	Leu	Arg	Leu	Pro	Asn 45	Leu	Glu	Ser
Phe	Val 50	Arg	Ala	Val	Lys	Asn 55	Leu	Glu	Asn	Ala	Ser 60	Gly	Ile	Glu	Ala
Ile 65	Leu	Arg	Asn	Leu	Gln 70	Pro	Cys	Leu	Pro	Ser 75	Ala	Thr	Ala	Ala	Pro 80
Ser	Arg	His	Pro	Ile 85	Ile	Ile	Lys	Ala	Gly 90	Asp	Trp	Gln	Glu	Phe 95	Arg

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
                   100                                  105                                  110  
 Gln

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1                                  5                                  10                                  15  
 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp  
                                   20                                  25                                  30  
 Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
                                   35                                  40                                  45  
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
                                   50                                  55                                  60  
 Ile Leu Arg Asn Leu Trp Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65                                  70                                  75                                  80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
                                   85                                  90                                  95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
                                   100                                  105                                  110  
 Gln

(2) INFORMATION FOR SEQ ID NO:294:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys  
 1                                  5                                  10                                  15  
 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
                                   20                                  25                                  30  
 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
                                   35                                  40                                  45  
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala

50		55		60											
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Gln	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

## (2) INFORMATION FOR SEQ ID NO:295:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Gln	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

## (2) INFORMATION FOR SEQ ID NO:296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp  
                   20                  25                  30

Val Asp Ile Leu Met Asp Arg Asn Leu Arg Leu Ser Asn Leu Glu Ser  
                   35                  40                  45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
           50                  55                  60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
   65                  70                  75                  80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
                   85                  90                  95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
                   100                  105                  110

Gln

## (2) INFORMATION FOR SEQ ID NO:297:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
   1                  5                  10                  15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
                   20                  25                  30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
           35                  40                  45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
           50                  55                  60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
   65                  70                  75                  80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
                   85                  90                  95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
                   100                  105                  110

Gln

## (2) INFORMATION FOR SEQ ID NO:298:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Ser	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:300:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys
1				5				10						15	
Arg	Pro	Pro	Ala	Pro	Ser	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
			20					25					30		
Met	Ser	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5				10						15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
			20					25					30		
Met	Ser	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
                             85                            90                            95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
                             100                            105                            110

Gln

## (2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 113 amino acids  
     (B) TYPE: amino acid  
     (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys  
   1                            5                            10                            15

Val Pro Pro Arg Pro Ser Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
                             20                            25                            30

Val Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
                             35                            40                            45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
                             50                            55                            60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
   65                            70                            75                            80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
                             85                            90                            95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
                             100                            105                            110

Gln

## (2) INFORMATION FOR SEQ ID NO:303:

- (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 113 amino acids  
     (B) TYPE: amino acid  
     (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
   1                            5                            10                            15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp  
                             20                            25                            30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser



	35		40		45										
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Arg	Met	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

## (2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Trp	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Arg	Met	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

## (2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
 20 25 30  
 Val Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
 35 40 45  
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln

## (2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys  
 1 5 10 15  
 Val Pro Pro Arg Pro Ser Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
 20 25 30  
 Val Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
 35 40 45  
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln

## (2) INFORMATION FOR SEQ ID NO:307:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Gln	Phe	Tyr	Leu	Val	Thr	Leu	Glu					
			100					105							

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

## (2) INFORMATION FOR SEQ ID NO:309:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1           5           10           15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
          20           25           30
Val Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
          35           40           45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
          50           55           60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65           70           75           80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
          85           90           95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
          100          105          110
Gln

```

## (2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1           5           10           15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
          20           25           30
Met Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
          35           40           45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
          50           55           60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65           70           75           80

```

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
                             85                            90                            95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
                             100                            105                            110

Gln

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys  
 1                            5                            10                            15

Arg Pro Pro Ala Pro Ser Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
                             20                            25                            30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Ser Asn Leu Glu Ser  
                             35                            40                            45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
                             50                            55                            60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65                            70                            75                            80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
                             85                            90                            95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
                             100                            105                            110

Gln

(2) INFORMATION FOR SEQ ID NO:312:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys  
 1                            5                            10                            15

Arg Pro Pro Ala Pro Ser Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
                             20                            25                            30

Met Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser

	35		40		45												
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala		
50						55					60						
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro		
65					70					75					80		
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg		
				85					90					95			
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln		
			100					105					110				
Gln																	

## (2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
50						55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Gln	Phe	Tyr	Leu	Trp	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

## (2) INFORMATION FOR SEQ ID NO:314:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Met	Asp	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

## (2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 125 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Met	Ala	Tyr	Pro	Glu	Thr	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Asn	Cys
1				5					10					15	
Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	Pro	Ala
			20					25					30		
Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp	Val	Asp	Ile	Leu
		35					40					45			
Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	Arg	Ala
	50					55					60				
Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	Arg	Asn
65					70					75					80
Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	His	Pro
			85					90						95	
Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	Leu	Thr
			100					105					110		
Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln			
		115					120					125			

## (2) INFORMATION FOR SEQ ID NO:316:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Met	Ala	Tyr	Pro	Glu	Thr	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Asn	Cys	1	5	10	15
Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	Pro	Asn	20	25	30	
Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp	Met	Asp	Ile	Leu	35	40	45	
Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala	Phe	Val	Arg	Ala	50	55	60	
Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	Arg	Asn	65	70	75	80
Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	His	Pro	85	90	95	
Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	Leu	Thr	100	105	110	
Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	115	120	125				

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Met	Ala	Asn	Cys	Ser	Ile	Met	Pro	Asp	Glu	Ala	Ile	His	His	Leu	Lys	1	5	10	15
Ile	Pro	Pro	Asn	Pro	Ser	Leu	Asp	Ser	Ala	Asn	Leu	Asn	Ser	Glu	Asp	20	25	30	
Val	Ser	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	85	90	95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	100	105	110	



Gln

## (2) INFORMATION FOR SEQ ID NO:318:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Leu	Ile	His	His	Leu	Lys	1	5	10	15
Ile	Pro	Pro	Asn	Pro	Ser	Leu	Asp	Ser	Ala	Asn	Leu	Asn	Ser	Glu	Asp	20	25	30	
Val	Ser	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	85	90	95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	100	105	110	

Gln

## (2) INFORMATION FOR SEQ ID NO:319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys	1	5	10	15
Ile	Pro	Pro	Asn	Pro	Ser	Leu	Asp	Ser	Ala	Asn	Leu	Asn	Ser	Glu	Asp	20	25	30	
Val	Ser	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Pro	50	55	60	

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80

Ser Arg Thr Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110

Gln

## (2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Met Ala Asn Cys Ser Ile Ile Leu Asp Glu Ala Ile His His Leu Lys  
 1 5 10 15

Ile Pro Pro Asn Pro Ser Leu Asp Ser Ala Asn Leu Asn Ser Glu Asp  
 20 25 30

Val Ser Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
 35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Pro  
 50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80

Ser Arg Thr Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110

Gln

## (2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp

	20		25		30	
Met	Asp	Ile	Leu	Met	Asp	Ser
	35				40	
Asn	Leu	Arg	Thr	Pro	Asn	Leu
					45	Leu
Ala						
Phe	Pro	His	Ala	Ser	Lys	Gln
	50				55	
Leu	Glu	Asn	Ala	Ser	Gly	Ile
					60	Glu
Ala						
Ile	Leu	Arg	Asn	Leu	Gln	Pro
					70	Cys
Leu	Pro	Ser	Ala	Thr	Ala	Ala
					75	Pro
Pro						
Ser	Arg	His	Pro	Ile	Ile	Lys
					85	Ala
Gly	Asp	Trp	Gln	Glu	Phe	Arg
					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu
					100	Val
Thr	Leu	Glu	Gln	Ala	Gln	Glu
					110	Gln
Gln						

## (2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5				10						15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
			35				40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
					70					75				80	
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
					85				90					95	
Leu	Lys	Leu	Gln	Phe	Tyr	Leu	Ser	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

## (2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Leu	Lys	Leu	Gln	Phe	Tyr	Leu	Ser	Thr	Leu						
			100					105							

## (2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Leu	Lys	Leu	Gln	Phe	Tyr	Leu	Ser	Ser	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100				105						110		

Gln

## (2) INFORMATION FOR SEQ ID NO:325:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Asp	Ser	Asn	Leu	Leu	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Pro	His	Ala	Ser	Lys	Gln	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Leu	Lys	Leu	Gln	Phe	Tyr	Leu	Ser	Ser	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Pro
	50					55					60				
Ile	Leu	Ser	Asn	Leu	Gln	Pro	Cys	Val	Pro	Tyr	Trp	Thr	Ala	Pro	Pro
65					70					75					80
Ser	Arg	Thr	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5				10						15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20				25						30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
	35						40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Pro
	50					55					60				
Ile	Leu	Ser	Asn	Leu	Gln	Pro	Cys	Val	Pro	Tyr	Trp	Thr	Ala	Pro	Pro
65					70					75				80	
Ser	Arg	Thr	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Leu	Lys	Leu	Gln	Phe	Tyr	Leu	Ser	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Leu	Ile	His	His	Leu	Lys
1				5				10						15	
Ile	Pro	Pro	Asn	Pro	Ser	Leu	Asp	Ser	Ala	Asn	Leu	Asn	Ser	Glu	Asp
			20				25						30		
Val	Ser	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Pro
	50					55					60				

Ile Leu Ser Asn Leu Gln Pro Cys Val Pro Tyr Trp Thr Ala Pro Pro  
65 70 75 80  
Ser Arg Thr Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95  
Leu Lys Leu Gln Phe Tyr Leu Ser Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110  
Gln

(2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Leu Ile His His Leu Lys  
1 5 10 15  
Ile Pro Pro Asn Pro Ser Leu Asp Ser Ala Asn Leu Asn Ser Glu Asp  
20 25 30  
Val Ser Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
35 40 45  
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60  
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80  
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95  
Leu Lys Leu Gln Phe Tyr Leu Ser Ser Leu Glu Gln Ala Gln Glu Gln  
100 105 110  
Gln

(2) INFORMATION FOR SEQ ID NO:330:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Leu Ile His His Leu Lys  
1 5 10 15  
Ile Pro Pro Asn Pro Ser Leu Asp Ser Ala Asn Leu Asn Ser Glu Asp

	20		25		30										
Val	Ser	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
	35						40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Pro
	50					55					60				
Ile	Leu	Ser	Asn	Leu	Gln	Pro	Cys	Val	Pro	Tyr	Trp	Thr	Ala	Pro	Pro
65					70					75					80
Ser	Arg	Thr	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

## (2) INFORMATION FOR SEQ ID NO:331:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys
1				5				10						15	
Arg	Pro	Pro	Ala	Pro	Ser	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
			20					25					30		
Met	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Ser	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

## (2) INFORMATION FOR SEQ ID NO:332:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

ATGGCAAAC	GCTCTATAGC	TATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCC	GAAGACATGG	ATATCCTGAT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

## (2) INFORMATION FOR SEQ ID NO:333:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

ATGGCAAAC	GCTCTATAAT	CATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCC	GAAGACATGG	ATATCCTGAT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

## (2) INFORMATION FOR SEQ ID NO:334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

ATGGCTAACT	GCTCTATAAT	GATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGAT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACGACG	300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG

339

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

ATGGCAAAC	GCTCTATAGC	TATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGAT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

ATGGCAAAC	GCTCTATAAT	GATCCATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGAT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT CGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:338:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGCT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:339:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGGA CGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:340:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

ATGGCAAAC	GCTCTATAGC	TATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGAT	CGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

ATGGCAAAC	GCTCTATAAT	CATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGAT	CGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEQ ID NO:342:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

[illegible]

ATGGCAAAC	T GCTCTATAGC	TATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGCT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACCTGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

ATGGCAAAC	TGCTCTATAAT	CATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGCT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACCTGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEO ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

ATGGCAAAC	TCTCTATAGC	TATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGGA	CGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACCTGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

ATGGCAAAC	GCTCTATAAT	CATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGGA	CGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCGGGA	AAAAC TGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEQ ID NO:346:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

ATGGCTAACT	GCTCTATTAT	GATCGATGAA	GCAATACATC	ACTTAAAGGT	TCCACCTGCA	60
CCTTTGCTGG	ACAGTAACAA	CCTCAATTCC	GAAGACATGG	ATATCCTGAT	GGAACGAAAC	120
CTTCGACTTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGAACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCGGGA	AAAAC TGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

ATGGCTAACT	GCTCTATAAT	GATCGATGAA	GCAATACATC	ACTTAAAGGT	TCCACCTGCA	60
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CCTTTGCTGG ACAGTAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC 120  
 CTTCGACTTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGCAA 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTTT CTATTCTGAT GGACCGAAAC 120  
 CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATAAC GAAGACGTTT CTATTCTGAT GGACCGAAAC 120  
 CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTTT CTATTCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:351:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTTT CTATTCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACATGT CTATTCTGAT GGACCGAAAC	120



CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACATGT CTATTCTGAT GGACCGAAAC 120  
 CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC 120  
 CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA G	321

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

ATGGATAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGCAA	300
TTCTATCTGG TTACCCTTGA G	321

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATTCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGCAA 300  
 TTCTATCTGG TTACCCTTGA G 321

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC 120  
 CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCTTGA G 321

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTTT CTATCCTGAT GGACCGAAAC 120  
 CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGCAA 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGGT ACCACCTCGC	60
CCTTCCCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCTGG CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTTT CTATTCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGCAA 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC 120  
 CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGCAA 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGACCGAAAC 120  
 CTTCGACTTA GCAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTCCCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG

339

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTCCCTGG ACCCGAACAA CCTCAATGAC GAAGACATGT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACATGT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGGT ACCACCTCGC	60
CCTTCCCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:371:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCT ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CCGTATGGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:372:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCT ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCTGG CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CCGTATGGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339



## (2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:374:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGGT ACCACCTCGC	60
CCTTCCCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:375:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 321 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGCAA	300
TTCTATCTGG TTACCCTTGA G	321

(2) INFORMATION FOR SEQ ID NO:376:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:377:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCG ATTCTCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCA TGTCTCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGAC	60
CTTTCCCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTA GCAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA	60
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CCTTCCCTGG ACCCGAACAA CCTCAATGAC GAAGACATGT CTATCCTGAT GGACCGAAAC 120  
 CTTCGACTTA GCAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA 60  
 CCTTCCCTGG ACCCGAACAA CCTCAATGAC GAAGACATGT CTATCCTGAT GGACCGAAAC 120  
 CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:382:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC 120  
 CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGCAA 300  
 TTCTATCTGT GGACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:383:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

ATGGATAACT GCTCTATTAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:384:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

ATGGCTAACT GCTCTATAAT GCCAGATGAA GCAATACATC ACTTAAAGAT ACCACCTAAC	60
CCTAGCCTGG ACAGTGCTAA CCTCAATTCC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:385:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAT ACCACCTAAC	60
CCTAGCCTGG ACAGTGCTAA CCTCAATTCC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:386:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

ATGGCTAACT GCTCTATTAT GATCGATGAA GCAATACATC ACTTAAAGAT ACCACCTAAC	60
CCTAGCCTGG ACAGTGCTAA CCTCAATTCC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:387:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

ATGGCTAACT GCTCTATAAT ACTCGATGAA GCAATACATC ACTTAAAGAT ACCACCTAAC	60
CCTAGCCTGG ACAGTGCTAA CCTCAATTCC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

## (2) INFORMATION FOR SEQ ID NO:388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGACTCCAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCCCA CATGCTGTCA AGCAATTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 339 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGACTCCAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCCCA CATGCTTCTA AGCAATTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 339 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCTGA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGCT TAAACTGCAA 300  
 TTCTATCTGT CTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC 120  
 CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGCT TAAACTGCAA 300  
 TTCTATCTGT CTACCCTT 318

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC 120  
 CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGCT TAAACTGCAA 300  
 TTCTATCTGT CTTCTCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGC CAATTCTTTC TAATCTCCAA CCATGTGTTC CCTATTGGAC GGCCCCCTCCC	240
TCTCGAACAC CAATCACGAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGC CAATTCTTTC TAATCTCCAA CCATGTGTTC CCTATTGGAC GGCCCCCTCCC	240
TCTCGAACAC CAATCACGAT CAAGGCAGGT GACTGGCAAG AATTCCGGCT TAAACTGCAA	300
TTCTATCTGT CTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:395:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAT ACCACCTAAC	60
CCTAGCCTGG ACAGTGCTAA CCTCAATTCC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGC CAATTCTTTC TAATCTCCAA CCATGTGTTC CCTATTGGAC GGCCCCCTCCC	240

TCTCGAACAC CAATCACGAT CAAGGCAGGT GACTGGCAAG AATTCCGGCT TAAACTGCAA 300  
 TTCTATCTGT CTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAT ACCACCTAAC 60  
 CCTAGCCTGG ACAGTGCTAA CCTCAATTCC GAAGACGTCT CTATCCTGAT GGAACGAAAC 120  
 CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGCT TAAACTGCAA 300  
 TTCTATCTGT CTTCTCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAT ACCACCTAAC 60  
 CCTAGCCTGG ACAGTGCTAA CCTCAATTCC GAAGACGTCT CTATCCTGAT GGAACGAAAC 120  
 CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180  
 GGTATTGAGC CAATTCTTTC TAATCTCCAA CCATGTGTTC CCTATTGGAC GGCCCCCTCCC 240  
 TCTCGAACAC CAATCACGAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:398:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG	60
CCGCTGCTGG ACTTCAACAA CCTCAATGAC GAAGACATGT CTATCCTGAT GGACAATAAC	120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA	180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC	240
ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC	300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAG	339

## (2) INFORMATION FOR SEQ ID NO:399:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG	60
CCGCTGCTGG ACTTCAACAA CCTCAATGAC GAAGACATGT CTATCCTGAT GGAAAATAAC	120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA	180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC	240
ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC	300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAG	339

## (2) INFORMATION FOR SEQ ID NO:400:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

AAGGAGATAT ATCCATGAAC TGCTCTAAC	29
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## (2) INFORMATION FOR SEQ ID NO:401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Met Asn Cys Ser Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln
1				5					10					15	
Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln
			20					25					30		
Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe
		35					40					45			
Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile
	50					55				60					
Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr
65					70					75				80	
Arg	His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg
				85					90					95	
Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln
			100					105					110		
Thr	Thr	Leu	Arg	Leu	Ala	Ile	Phe								
		115				120									

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Met Ala Tyr Pro Glu Thr Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

ATGGCATATC CAGAAACTGA TTACAAGGAC GACGATGACA AGGCTAACTG CTCTATAATG	60
ATCGATGAAA TTATACATCA CTTAAAGAGA CCACCTGCAC CTTTGCTGGA CCCGAACAAC	120
CTCAATGCTG AAGACGTCGA TATCCTGATG GAACGAAACC TTCGACTTCC AAACCTGGAG	180
AGCTTCGTAA GGGCTGTCAA GAACTTAGAA AATGCATCAG GTATTGAGGC AATTCTTCGT	240
AATCTCCAAC CATGTCTGCC CTCTGCCACG GCCGCACCCT CTCGACATCC AATCATCATC	300
AAGGCAGGTG ACTGGCAAGA ATTCCGGGAA AAACCTGACGT TCTATCTGGT TACCCTTGAG	360
CAAGCGCAGG AACAACAG	378

(2) INFORMATION FOR SEQ ID NO:405:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 378 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

ATGGCATATC CAGAAACTGA TTACAAGGAC GACGATGACA AGGCTAACTG CTCTATAATG	60
ATCGATGAAA TTATACATCA CTTAAAGAGA CCACCTAACC CTTTGCTGGA CCCGAACAAC	120
CTCAATTCCG AAGACATGGA TATCCTGATG GAACGAAACC TTCGAACTCC AAACCTGCTC	180
GCATTCGTAA GGGCTGTCAA GCACTTAGAA AATGCATCAG GTATTGAGGC AATTCTTCGT	240
AATCTCCAAC CATGTCTGCC CTCTGCCACG GCCGCACCCT CTCGACATCC AATCATCATC	300
AAGGCAGGTG ACTGGCAAGA ATTCCGGGAA AAACCTGACGT TCTATCTGGT TACCCTTGAG	360
CAAGCGCAGG AACAACAG	378

(2) INFORMATION FOR SEQ ID NO:406:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys

1		5		10		15
Gln	Pro	Pro	Leu	Pro	Leu	Leu
			20			25
						30
Met	Ser	Ile	Leu	Met	Glu	Asn
		35				40
						45
Phe	Asn	Arg	Ala	Val	Lys	Ser
						55
						60
Ile	Leu	Lys	Asn	Leu	Leu	Pro
65					70	
						75
Thr	Arg	His	Pro	Ile	Ile	Arg
						85
						90
Arg	Lys	Leu	Thr	Phe	Tyr	Leu
						100
						105
						110
Gln						

(2) INFORMATION FOR SEQ ID NO:407:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1				5					10					15	
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
			20					25					30		
Ile	Leu	Met	Asp	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
		35					40					45			
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu
		50				55					60				
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg
65					70				75					80	
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys
				85					90					95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:408:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG 60  
 CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTGAT GGAACAATAA 120  
 CCTTCGTCGT CCAAACCTCG AGGCATTCAA CCGTGCTGTC AACTCTCTGC AGAATGCATC 180  
 AGCAATTGAG AGCATTCTTA AAAATCTCCT GCCATGTCTG CCCCTGGCCA CGGCCGCACC 240  
 CACGCGACAT CCAATCCATA TCAAGGACGG TGA CTGGAAT GAATTCGTC GTAAACTGAC 300  
 CTTCTATCTG AAAACCTTGG AGAACGCGCA GGCTCAACAG 340

## (2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 45 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

CTTTAAGTGA TGTATAATTT CATCGATCAT TATAGAGCAG TTAGC 45

## (2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

CACTTAAAGA GACCACCTGC ACCTTTGCTG GACCCG 36

## (2) INFORMATION FOR SEQ ID NO:411:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

GAGGTTGTTC GGGTCCAGCA AAGGTGCAGG TGGTCT 36

## (2) INFORMATION FOR SEQ ID NO:412:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

CACTTAAAGA GACCACCTAA CCCTTTGCTG GACCCG

36

(2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GAGGTTGTTC GGGTCCAGCA AAGGGTTAGG TGGTCT

36

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

CACTTAAAGG TTCCACCTGC ACCTTTGCTG GACAGT

36

(2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GAGGTTGTTA CTGTCCAGCA AAGGTGCAGG TGGAAC

36